

43540

Delavai, Jan

From: Roark, Jessica
Sent: Wednesday, May 30, 2001 4:39 PM
To: Delavai, Jan
Subject: 09/509,283

Jan,

Please search, including interference,

SEQ ID NO:2
SEQ ID NO:2 as an oligo search

Results on paper and disk please.

Thanks!

Jessica H. Roark

CM1 9B03
Mailbox 9E12
Art Unit 1644
703 605-1209

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GenCore version 4.5
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OM protein - protein search, using sw model

Run On: May 30, 2001, 16:49:03 ; Search time 19.73 Seconds
(without alignments)
573.660 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 1078
Sequence: 1 MKSGLMYFFFLCRLRVLTG.....YMEKAVNTRAKKSLDVTYL 198

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 0401.*
1: /SID56/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SID56/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SID56/gcgdata/geneseq/geneseq/AA1982.DAT:*
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21: /SID56/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SID56/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result NO. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|----------------------------|
| 1 | 1067.5 | 99.0 | 199 | 19 | W75956 Human cell surface |
| 2 | 1067.5 | 99.0 | 199 | 19 | W75957 Human cell surface |
| 3 | 1067.5 | 99.0 | 199 | 20 | Y08026 Human activated T- |
| 4 | 1067.5 | 99.0 | 199 | 21 | B08731 Amino acid sequenc |
| 5 | 1052 | 97.6 | 198 | 21 | Y92213 Human TH2-specific |
| 6 | 727 | 67.4 | 200 | 21 | Y92212 Murine TH2-specific |
| 7 | 723.5 | 67.1 | 200 | 21 | B08723 Amino acid sequenc |
| 8 | 712 | 66.0 | 200 | 19 | W75958 Mouse cell surface |
| 9 | 695.5 | 64.5 | 200 | 19 | W71874 Rat cell surface p |
| 10 | 690.5 | 64.1 | 216 | 19 | W71875 Rat cell surface p |
| 11 | 143 | 13.3 | 225 | 20 | Y41136 Rat CD28 protein s |

| | | | | | |
|----|-------|------|-----|----|---------------------------|
| 12 | 141 | 13.1 | 221 | 21 | Y32286 Feline CD28, fel |
| 13 | 141 | 13.1 | 221 | 21 | Y32279 Cat CD28 receptor. |
| 14 | 136 | 12.6 | 220 | 13 | R20805 Human CD28 antigen |
| 15 | 136 | 12.6 | 220 | 13 | R27103 Sequence encoded b |
| 16 | 136 | 12.6 | 220 | 17 | W02131 Human CD28 cDNA pr |
| 17 | 136 | 12.6 | 220 | 17 | R91433 Human CD28 antigen |
| 18 | 136 | 12.6 | 220 | 18 | M38413 CD28. Homo sapien |
| 19 | 136 | 12.6 | 220 | 19 | W80442 Human CD28 antigen |
| 20 | 136 | 12.6 | 220 | 20 | W88451 Human CD28 antigen |
| 21 | 136 | 12.6 | 220 | 21 | Y96128 Human cell surface |
| 22 | 136 | 12.6 | 220 | 21 | Y44294 Human CD28 recepto |
| 23 | 129.5 | 12.0 | 225 | 20 | Y41135 Mouse CD28 protein |
| 24 | 121.5 | 11.3 | 223 | 20 | Y41137 Human CD28 protein |
| 25 | 120.5 | 11.2 | 367 | 18 | W35862 Human CD28:19G2a c |
| 26 | 119.5 | 11.1 | 134 | 18 | W35846 Human CD28 for use |
| 27 | 119.5 | 11.1 | 152 | 16 | R67706 CD28 extracellular |
| 28 | 89.5 | 8.3 | 117 | 20 | Y24469 Human CD28 gene pr |
| 29 | 86 | 8.0 | 635 | 20 | Y24321 Mouse dephosphoryl |
| 30 | 86 | 8.0 | 663 | 20 | Y24322 Mouse dephosphoryl |
| 31 | 85.5 | 7.9 | 223 | 18 | W25111 Soluble human CTLA |
| 32 | 85 | 7.9 | 187 | 19 | W29728 Soluble CTLA4 muta |
| 33 | 84.5 | 7.8 | 226 | 20 | Y41138 Chicken CD28 prote |
| 34 | 84 | 7.8 | 229 | 11 | R04495 HIV fusion protein |
| 35 | 83.5 | 7.7 | 223 | 21 | Y15129 Human CTLA-4 prote |
| 36 | 83 | 7.7 | 209 | 21 | Y94998 Human secreted pro |
| 37 | 81.5 | 7.6 | 330 | 8 | P70445 Sequence of mouse |
| 38 | 81 | 7.5 | 187 | 17 | R86945 Human T cell speci |
| 39 | 81 | 7.5 | 187 | 20 | Y41130 CTLA4 receptor wit |
| 40 | 81 | 7.5 | 187 | 20 | W97615 Human CTLA recepto |
| 41 | 81 | 7.5 | 187 | 20 | W97610 Human CTLA recepto |
| 42 | 81 | 7.5 | 211 | 20 | W87560 Human CTLA4 recept |
| 43 | 81 | 7.5 | 212 | 14 | R31040 Human CTLA4 recept |
| 44 | 81 | 7.5 | 212 | 15 | R60134 CTLA4 receptor fus |
| 45 | 81 | 7.5 | 212 | 16 | R77642 Full length CTLA4 |

ALIGNMENTS

| | |
|----------------|---|
| RESULT 1 | |
| ID W75956 | standard; Protein: 199 AA. |
| XX W75956; | |
| XX 11-DEC-1998 | (first entry) |
| XX | |
| XX | Human cell surface protein #1. |
| DE | |
| XX | |
| KW | Human; cell surface protein; thymocyte; lymphocyte; cell adhesion; |
| KW | signal transduction; autoimmune disorder; allergy; diagnosis; |
| KW | mitogen-stimulated. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | W09838216-A1. |
| XX | |
| PD | 03-SEP-1998. |
| XX | |
| PF | 27-FEB-1998; 98WO-JP00837. |
| XX | |
| PR | 26-FEB-1998; 98JP-0062217. |
| XX | |
| PR | 27-FEB-1997; 97JP-0062290. |
| XX | |
| PA | (NISR) JAPAN TOBACCO INC. |
| XX | |
| PI | Tamabani T, Tezuka K; |
| XX | |
| DR | WPI: 1998-481144/41. |
| XX | |
| DR | N-PSDB: V53198. |
| XX | |
| PT | Cell surface molecule expressed in thymocytes and lymphocytes and - |
| | mediating signal transduction and cell adhesion, and antibodies to |

PT It useful in treatment of auto:immune and allergic disorders.
 XX
 PS Claim 2; Page 99-101; 149pp; Japanese.
 XX
 CC The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognizing the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FDKPPF in its extracellular region and the
 CC sequence YWFM in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 XX
 SO Sequence 199 AA;

Query Match 99.0%; Score 1067.5; DB 19; Length 199;
 Best Local Similarity 99.5%; Pred. No. 8.6e-113;
 Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 MKSGIWFYFFLCRIKVLTEGEINGSANYEMFIFHNGVQILCKYPIVQGFQKMLKGGQ 60
 1 mksglwyfflfcrlrkvltegeingsanyemfifhngvqilckypdivqgfkmqllkqgq 60
 Db 1 mksglwyfflfcrlrkvltegeingsanyemfifhngvqilckypdivqgfkmqllkqgq 60

61 ILCDLRTKSGMNTVSIKSLKFCQSLSNNSVSFFLYNLDSHANYFCNLSTFDPPEK 120
 61 ilcdlrtksgmntvsikslkfcqslnnsvsfflynlldshanyfcnlstfdppfk 120
 Db 61 ilcdlrtksgmntvsikslkfcqslnnsvsfflynlldshanyfcnlstfdppfk 120

121 VTLTGGLIHYESQLCCQLKFWLPICGAAF-VYCILGLCILICWLTKKKSSSVHDPNGEY 179
 121 vtltgglihyesqlccqlkfwlpigcaafvvcilgclilcwltkkkyssvhdnpney 180
 Db 121 vtltgglihyesqlccqlkfwlpigcaafvvcilgclilcwltkkkyssvhdnpney 180

180 MFMRAVNTAKKSRLTDVTL 198
 180 mfmravntakksrltdvtl 199
 Db 181 mfmravntakksrltdvtl 199

RESULT 2
 W75957
 ID W75957 standard; Protein; 199 AA.
 XX
 AC W75957;
 XX
 DT 11-DEC-1998 (first entry)
 XX
 DE Human cell surface protein #2.
 XX
 KW Human; cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transduction; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 OS Homo sapiens.
 XX
 PN WO9838216-A1.
 XX
 PD 03-SEP-1998.
 XX
 PF 27-FEB-1998; 98WO-JP00837.
 XX
 PR 26-FEB-1998; 98JP-0062217.
 XX
 PR 27-FEB-1997; 97JP-0062290.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 XX
 PI Tamatani T, Tezuka K;
 XX
 DR WPI; 1998-481144/41.
 XX
 DR N-PSDB; V53199.
 XX
 PT Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transduction and cell adhesion, and antibodies to

PT It useful in treatment of auto:immune and allergic disorders.
 XX
 PS Claim 9; Page 101-105; 149pp; Japanese.
 XX
 CC The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognizing the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FDKPPF in its extracellular region and the
 CC sequence YWFM in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 XX
 SO Sequence 199 AA;

Query Match 99.0%; Score 1067.5; DB 19; Length 199;
 Best Local Similarity 99.5%; Pred. No. 8.6e-113;
 Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 MKSGIWFYFFLCRIKVLTEGEINGSANYEMFIFHNGVQILCKYPIVQGFQKMLKGGQ 60
 1 mksglwyfflfcrlrkvltegeingsanyemfifhngvqilckypdivqgfkmqllkqgq 60
 Db 1 mksglwyfflfcrlrkvltegeingsanyemfifhngvqilckypdivqgfkmqllkqgq 60

61 ILCDLRTKSGMNTVSIKSLKFCQSLSNNSVSFFLYNLDSHANYFCNLSTFDPPEK 120
 61 ilcdlrtksgmntvsikslkfcqslnnsvsfflynlldshanyfcnlstfdppfk 120
 Db 61 ilcdlrtksgmntvsikslkfcqslnnsvsfflynlldshanyfcnlstfdppfk 120

121 VTLTGGLIHYESQLCCQLKFWLPICGAAF-VYCILGLCILICWLTKKKSSSVHDPNGEY 179
 121 vtltgglihyesqlccqlkfwlpigcaafvvcilgclilcwltkkkyssvhdnpney 180
 Db 121 vtltgglihyesqlccqlkfwlpigcaafvvcilgclilcwltkkkyssvhdnpney 180

180 MFMRAVNTAKKSRLTDVTL 198
 180 mfmravntakksrltdvtl 199
 Db 181 mfmravntakksrltdvtl 199

RESULT 3
 Y08026
 ID Y08026 standard; Protein; 199 AA.
 XX
 AC Y08026;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE Human activated T-lymphocyte protein 8F4.
 XX
 KW T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;
 KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;
 KW T cell activation; cytokine synthesis; regulatory element; B cell;
 KW T cell-dependent antibody production; treatment; prevention; cancer;
 KW autoimmune disease; transplant rejection; immune system regulation;
 KW disorder; acquired immune deficiency syndrome; AIDS; asthma.
 XX
 OS Homo sapiens.
 XX
 PN WO9915553-A2.
 XX
 PD 01-APR-1999.
 XX
 PF 23-SEP-1998; 98WO-DE02896.
 XX
 PR 11-MAY-1998; 98DE-1021060.
 XX
 PR 23-SEP-1997; 97DE-1041929.
 XX
 PA (DEKO-) DEUT KOCH INST ROBERT.
 XX
 PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
 XX
 PI Kroczeck R;
 XX
 DR WPI; 1999-276975/23.

DR N-PSDB; X37661.
XX Polypeptide 8F4 co-stimulates T cells and is present only on
PT activated cells
XX
PS Claim 2; Page 24; 47pp; German.
XX
CC This invention describes a novel human protein, 8F4, and its encoding
CC nucleic acid which co-stimulates T cells and is present on activated CD4+
CC and CD8+ T cells but not on resting or activated B cells, granulocytes,
CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,
CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a
CC strong co-stimulatory signal for T cell activation, i.e. it amplifies
CC proliferation of T cells, synthesis of certain cytokines and other
CC regulatory agents, and improves T cell-dependent antibody production
CC by B cells. Agents that inhibit 8F4 are used to treat or prevent
CC autoimmune diseases, to prevent transplant rejection and to treat
CC disorders of immune system regulation. 8F4, or cells that express it,
CC is/are used to treat or prevent cancers, acquired immune deficiency
CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).
XX
SQ Sequence 199 AA:

Query Match 99.0%; Score 1067.5; DB 20; Length 199;
Best Local Similarity 99.5%; Pred. No. 8.6e-113;
Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 MKSGLYEFLFCRLRIKVLGEINGSANYEMFIFHNGVQIICKYDPIVQOFKMLLKGGQ 60
DB 1 mksqlywfflfcrlrikvltgelingsanyemifhngvqllckypdivqfkmqlkqg 60
OY 61 ILCDLTTRKGSNTVSIKSRCHSOLSNNSVFFLYLNDHSHANYFCNLSIDPPPEPK 120
DB 61 ilcdlttrkgsntvsiiksrfchsqslsnsvsfflylnshanyfcnlsidpppfk 120
OY 121 VLTGGLHIYESQCCOLKFWLPICGAAF-VVCILGCLICMLTKRKYSVHDNGEY 179
DB 121 vltggylhiyesqccqlkfwpigcaafvvcilgcllcmlltkrkyssvhdngyey 180
OY 180 MEMRAVNTAKRSRLTDVTL 198
DB 181 mfmravntakkerltdvcl 199

XX 4
XX ID B08731 standard; Protein; 199 AA.
XX AC B08731.
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human CRP1 polypeptide.
XX
KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
KW T-lymphocyte activation; type I transmembrane protein; T cell activation;
KW T cell proliferation; T-cell mediated disorder.
XX
XX Homo sapiens.
XX OS
XX
FH Key
FT Peptide
FT 1..20 Location/Qualifiers
FT /note- "signal peptide"
FT 21..199
FT /note- "mature protein"
FT 21..140
FT /note- "extracellular domain"
FT 141..161
FT /note- "predicted transmembrane domain"
FT 162..199
FT Domain
XX /note- "intracellular domain"
XX

PN W0200046240-A2.
XX
XX 10-AUG-2000.
XX
PD 27-JAN-2000; 2000WO-US01871.
XX
PF 03-FEB-1999; 99US-0244448.
XX 08-MAR-1999; 99US-0264527.
XX
PA (AMGE-) AMGEN INC.
XX
PI Yoshinaga SK;
XX WPI: 2000-543476/49.
XX N-PSDB; A64558.
DR
DR Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
PT in the treatment, prevention and diagnosis of T cell mediated disorders
PT
XX
PS Disclosure: Fig 13A; 174pp; English.
XX
XX The present sequence represents a CRP1 (CD28 related protein-1)
CC polypeptide. The specification also describes a B7RP1 (B7 related
CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
CC predicted to be a type I transmembrane protein. The nucleic acids are
CC useful for regulating T cell activation or proliferation in an animal.
CC The polypeptides are useful for treating, preventing ameliorating or
CC diagnosing a T-cell mediated disorder in an animal. They can also be
CC used to identify test molecules that bind to the polypeptides.
XX
SQ Sequence 199 AA:

Query Match 99.0%; Score 1067.5; DB 21; Length 199;
Best Local Similarity 99.5%; Pred. No. 8.6e-113;
Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 MKSGLYEFLFCRLRIKVLGEINGSANYEMFIFHNGVQIICKYDPIVQOFKMLLKGGQ 60
DB 1 mksqlywfflfcrlrikvltgelingsanyemifhngvqllckypdivqfkmqlkqg 60
OY 61 ILCDLTTRKGSNTVSIKSRCHSOLSNNSVFFLYLNDHSHANYFCNLSIDPPPEPK 120
DB 61 ilcdlttrkgsntvsiiksrfchsqslsnsvsfflylnshanyfcnlsidpppfk 120
OY 121 VLTGGLHIYESQCCOLKFWLPICGAAF-VVCILGCLICMLTKRKYSVHDNGEY 179
DB 121 vltggylhiyesqccqlkfwpigcaafvvcilgcllcmlltkrkyssvhdngyey 180
OY 180 MEMRAVNTAKRSRLTDVTL 198
DB 181 mfmravntakkerltdvcl 199

XX
XX RESULT 5
XX ID Y92213 standard; Protein; 198 AA.
XX AC Y92213.
XX
DT 10-AUG-2000 (first entry)
XX
DE Human Th2-specific polypeptide, h1228.
XX
KW h1228: Th2-specific; T helper cell; anti-inflammatory; antiarthritic;
KW CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;
KW antiproliferative; antiallergic; anti-viral; optalmatological;
KW CMTA-4; nephrotropic; anti-HIV; antibacterial.
XX
XX Homo sapiens.
XX

| | | | |
|----|--|--|--------------------------------|
| FH | Key | | Location/Qualifiers |
| FT | Peptide | 113..118 | /Label= conserved_ppp_motif |
| FT | | /note= "common in CD28 and CTLA-4" | |
| FT | Peptide | 178..181 | /label= YXXM_motif |
| FT | | /note= "common in CD28 and CTLA-4; necessary for CD28-mediated phosphatidylinositol 3-kinase activity" | |
| FX | | | |
| PN | | WO200019988-A1. | |
| PD | | 13-APR-2000. | |
| XX | | | |
| PF | | 06-OCT-1999; | 99WO-US23156. |
| XX | | | |
| PR | | 07-OCT-1998; | 98US-0168229. |
| XX | | | |
| PR | | 26-FEB-1999; | 99US-0258670. |
| XX | | | |
| PA | | 06-OCT-1999; | 99US-0413136. |
| XX | | (MILL-) MILLENNIUM PHARM INC. | |
| FX | | | |
| FX | Jehar S, Manning S, Coyle AJ, Gutierrez-Ramos J; | | |
| DR | WPI; 2000-303619/26. | | |
| DR | N-PSTB; A09056. | | |
| XX | | | |
| PS | Claim 16; Page 138-139; 159Pp; English. | | |
| CC | This Th2-specific polypeptide, which has similarity to human CD28 and human CTLA-4 is encoded by human orthologue h1228. | | |
| CC | A novel method for modulating a Th2 response, an immune response, or suppressing airway inflammation or hyperresponsiveness in a mammal comprises administering a Th2-specific polypeptide of the invention, an antibody to such a polypeptide or allelic variants of the genes. The novel DNA and polypeptide sequences are useful for treatment and diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases, arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis, dermatitis, psoriasis, graft rejection, graft versus host diseases, sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis, viral infections (including human immunodeficiency virus (HIV)), bacterial infections, bronchitis, cystic fibrosis, diphtheria, emphysema, pneumonia, and Legionnaires disease. | | |
| SO | Sequence 198 AA: | | |
| ■ | | | |
| | Early Match | 97.6%; | Score 1052; DB 21; Length 198; |
| | Best Local Similarity | 99.0%; | Pred. No. 4.9e-111; |
| | Matches 197; Conservative | 0; | Mismatches 0; Indels 2; Gaps 2 |
| OY | 1 MMSGLMYFFELFRLKRYLVGTEINGSNANYEMTFPHNGVQILCKRPDIYQOFKMQLKGQ | 60 | |
| DB | 1 mksqgwyfflflrltkvltvgelngasnyemfllhngvyqlckypdiyqfikmqdlkgyq | 60 | |
| OY | 61 ILCDLTKTSGSNTYSIKSLKFCHSOLSNNSVSFPFLYNLDHSNANYFCNLSTIFPPPK | 120 | |
| DB | 61 llcdltkctkgsgntvsyksikcfchgslmsnsfflylnldhsnanyfnlsiffpprk | 120 | |
| OY | 121 VTLGGYLHIYESQLCCLKEFWLPITGCANF-VVCIIICLITLCWLTKRKYSVVDPNGEY | 179 | |
| DB | 121 veltggylhiyesqlccqklfwlpigcaafvvvcilliclwilt-kkysssvdhpngey | 179 | |
| OY | 180 MEMRAVNAAKKSRIDVTLL | 198 | |
| DB | 180 mfmravnaakksrildvtllcavl | 198 | |

| | | |
|---------------------------|---|---|
| RESUT | T | 6 |
| ID | Y92212 | standard; Protein: 200 AA. |
| AC | Y92212; | |
| DT | 10-AUG-2000 | (first entry) |
| XX | Murine Th2-specific polypeptide, m128. | |
| DE | m1288: Th2-specific; T helper cell; anti-inflammatory; antiarthritic; CD28: antidiabetic; immunosuppressive; neuroprotective; dermatological; antipruritic; antisthmatic; antiallergic; anti-viral; ophthalmological; CTLA-4; nephrotoxic; anti-HIV; antibacterial. | |
| KM | Mus musculus. | |
| OS | | |
| XX | Key | Location/Qualifiers |
| FH | Peptide | 114..119 /Label'' conserved_PPP_motif |
| FT | | /note'' "common in CD28 and CTLA-4" |
| FT | Peptide | 181..184 /Label'' YXXM_motif |
| FT | | /note'' "xxxm in CD28 and CTLA-4; necessary for CD28-mediated phosphatidylinositol 3-kinase activity" |
| FT | | |
| PN | WO200019988-A1. | |
| PD | 13-APR-2000. | |
| PF | 06-OCT-1999; | 99WO-US23156. |
| PR | 07-OCT-1998; | 98US-0168229. |
| PR | 26-FEB-1999; | 99US-0258670. |
| PA | 06-OCT-1999; | 99US-0413136. |
| PI | (MILL-) MILLENNIUM PHARM INC. | |
| PJ | Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J; | |
| DR | WPI: 2000-303619/26. | |
| NFSD | N-PDB: A09054. | |
| PT | T helper (Th) 2 nucleic acids and encoded proteins, useful for the diagnosis and treatment of immune and respiratory disorders such as Crohn's disease, arthritis, insulin dependent diabetes and autoimmunity | |
| PS | Claim 16; Page 130-131; 159Pp; English. | |
| XX | This Th2-specific polypeptide is encoded by a murine orthologue m1288. The protein shares homology with both human and murine CD28 and CTLA-4. A novel method for modulating a Th2 response, an immune response, or suppressing airway inflammation or hyperresponsiveness in a mammal, comprising administering a Th2-specific polypeptide of the invention, an antibody to such a polypeptide or allelic variants of the genes. The novel DNA and polypeptide sequences are useful for treatment and diagnosis of Th cell and Th cell-like disorders such as Crohn's disease, arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis, dermatitis, psoriasis, graft rejection, graft versus host diseases, sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis, viral infections (including human immunodeficiency virus (HIV)), bacterial infections, bronchitis, cystic fibrosis, diphtheria, emphysema, pneumonia, and Legionnaires disease. | |
| SQ | Sequence | 200 AA: |
| Query Match | 67.4%; Score 727; | DB 21: Length 200; |
| Best Local Similarity | 69.3%; Pred. No. 2.9e-74; | |
| Matches 138: Conservative | 20; Mismatches 39; | Indels 2; Gaps 2 |

[illegible]

| | |
|--------|--|
| CC | The polypeptides are useful for treating, preventing ameliorating or |
| CC | diagnosing a T-cell mediated disorder in an animal. They can also be |
| CC | used to identify test molecules that bind to the polypeptides. |
| XX | |
| SQ | Sequence 200 AA; |
| OY | Query Match 67.1%; Score 723.5; DB 21; Length 200; |
| Db | Best Local Similarity 70.4%; Pred. No. 7,1e-74; |
| | Matches 138; Conservative 19; Mismatches 34; Indels 5; Gaps |
| OY | 7 YF---FLPCLRIKIVLGEINGSANYEMPLFEHNGGVGIICKYPDIVOGRMKLGSGIIC 63 |
| Db | 4 YFCRVIVFCILIRLIYELNgsadhmifsfmgvgqiskypetvqlkmlffereyic 63 |
| OY | 64 DLRTKGSGNTVSIKLSLKPCSHSOLSNNSVSFFLYNLDSHANYPNCNISIFDPEPFKY-T 122 |
| Db | 64 eltkktsgnavaishkpmcllylnsnsvsfflmpdsqsgysfcsisltdppfgern 123 |
| OY | 123 LTGGYLHIYESQLCCQLEKFWLPGLPCAFAVVCIL-GCILICWLTKKKSSSVHDNGETMF 181 |
| Db | 124 lsggylhiyesqlccqikilwlpvgcaafvvllfgcilliwfskkkyssvhdnpseymf 183 |
| OY | 182 MRAYVTAKKSRLTDYT 197 |
| Db | 184 maavtnkksrlagvt 199 |
| RESULT | 8 |
| W75958 | |
| ID | W75958 standard; Protein; 200 AA. |
| AC | |
| XX | W75958; |
| DT | 11-DEC-1998 (first entry) |
| XX | |
| DE | Mouse cell surface protein. |
| KW | Mouse; cell surface protein; thymocyte; lymphocyte; cell adhesion; |
| KW | signal transmission; autoimmune disorder; allergy; diagnosis; |
| XX | mitogen-stimulated. |
| OS | Mus sp. |
| XX | |
| PN | WO9838216-A1. |
| XX | |
| PD | 03-SEP-1998. |
| XX | |
| PP | 27-FEB-1998; 98WO-JP00837. |
| XX | |
| PR | 26-FEB-1998; 98JP-0062217. |
| XX | 27-FEB-1997; 97JP-0062290. |
| PA | (NISB) JAPAN TOBACCO INC. |
| XX | |
| PI | Tamatani T, Tezuka K; |
| DR | |
| DR | WPI: 1998-481144/41. |
| DR | N-PsDB: V53200. |
| XX | |
| PT | Cell surface molecule expressed in thymocytes and lymphocytes and - |
| PT | mediating signal transmission and cell adhesion, and antibodies to |
| XX | it useful in treatment of auto-immune and allergic disorders. |
| PS | Claim 9; Page 110-112; 149pp; Japanese. |
| XX | |
| CC | The present sequence represents a mouse cell surface protein which is |
| CC | expressed by thymocytes and by mitogen-stimulated lymphocytes. The cel |
| CC | surface protein induces adhesion of mitogen-stimulated lymphocytes to |
| CC | antibodies recognising the cell surface protein. These antibodies also |
| CC | produce an increase in peripheral blood lymphocytes in the presence of |
| CC | an antibody recognising CD3 antigen. The cell surface protein contains |
| CC | the amino acid sequence FDPPEF in its extracellular region and the |


```

FT Modified-site /label= N-linked_glycosylation
FT 71..73
FT Modified-site /label= N-linked_glycosylation
FT 92..94
FT Modified-site /label= N-linked_glycosylation
FT 105..107
FT Modified-site /label= N-linked_glycosylation
FT 129..131
FT Modified-site /label= N-linked_glycosylation
FT 153..179
FT Region /label= transmembrane
FT /label= transmembrane
PN WC9201049-A.
XX
XX
XX 23-JAN-1992.
XX
XX 15-JUL-1990; 90WO-US04986.
XX
XX 13-JUL-1990; 90US-0553759.
XX
XX (GEHO-) GEN HOSPITAL CORP.
XX
XX Seed B, Aruffo A, Amlot M;
XX
XX WPI: 1992-056864/07.
XX
XX N-PSDB; Q21167.
XX
XX New CD53 cell surface antigen and DNA encoding it - for
XX immuno-therapy and diagnosis of haematopoietic neoplasms, etc.
XX
XX Example 3; Fig 7; 160pp; English.
XX
XX The CD28 antigen amino acid sequence was predicted from the
XX nucleotide sequence of a cDNA clone isolated from a human
XX lymphoblastoid cell line JY library using the antibody enrichment
XX method (see Q21167). The sequence of the CD28 antigen has
XX substantial homology with mouse and rabbit immunoglobulin
XX heavy-chain variable regions over a domain spanning almost the
XX entire extracellular portion of CD28.
XX
XX Sequence 220 AA;
SQ
Query Match 12.6%; Score 136; DB 13; Length 220;
Best Local Similarity 24.6%; Pred. No. 2.3e-07;
Matches 42; Conservative 31; Mismatches 76; Indels 22; Gaps 7;
QY 30 MFIHNGVQILCKYPD--IVQEFKMLKGGQILCDLTKRSGN--TVSIRSLKRFCH 84
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 28 mlvaydnavnlsckysynlfrefraihkgldasavevcvnygsqlyysktgfncd 87
QY 85 SOLSNNSVSFFLYNLIDSHANYFCNLSIFDPPFP--KVTLTGGLHYESQLC----- 136
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 88 gklgnesvtlylqnlvnyqtdlyfcklevmypypldneksngtlhvkghkhlcpstlfp 147
QY 137 -COLKFWLPICACAFVVC---ILGCLILCWLTKKRYSSVHDPNGEYFM 182
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 148 gpskpfwlvvvgvylacysllvtvaflifwvrskr-slllh---sdyymm 194
RESULT 15
R27103
ID R27103 standard; Protein; 220 AA.
XX
XX R27103;
XX
XX 25-FEB-1993 (first entry)
XX
XX Sequence encoded by the CD28 gene.
XX
XX CD28 protein; T-cell immune response; Tp44; differentiation antigen;
XX membrane protein.
XX

```

```

OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..18
XX /label= signal
XX Region 153..179
XX /label= Transmembrane region
XX
XX WC9215671-A.
XX
XX 17-SEP-1992.
XX
XX 09-MAR-1992; 92WO-US01867.
XX
XX 08-MAR-1991; 91US-0666809.
XX
XX (CYTO-) CYTOMED INC.
XX
XX KO JL, IP SH;
XX
XX WPI: 1992-331717/40.
XX
XX N-PSDB; Q28837.
XX
XX Soluble proteins binding to B7 proteins and block antigen presenting
XX cells - are useful in treating T-cell mediated immunosuppression
XX diseases e.g. transplant rejection, autoimmune diseases etc.
XX
XX Disclosure; Fig 1; 43pp; English.
XX
XX The cDNA sequence in Q28837 is derived from Aruffo A and Seed B,
XX PNAS USA 84, 8573-77, 1987. The CD28 cDNA encodes a protein of 220
XX AAs (R27103). It contains a signal peptide from AAs 1-18 which is
XX cleaved during the maturation of CD28 protein. The transmembrane
XX region is AAs 153-79. For the production of soluble CD28 protein,
XX the transmembrane region is deleted. The CD28 protein derived from
XX p9-MIT comprises residues 19-157 and is not soluble; the CD28
XX protein derived from p9-CIT comprises residues 19-151 and is soluble.
XX MIT and CIT are primers. T7 primer is used as the 5' primer to pair
XX with any 3' primer, eg, MIT and CIT, in a PCR reaction for the
XX procurement of truncated CD28 gene which would direct the production
XX of soluble CD28 protein. A compound containing residues 19-151 of
XX CD28 protein is claimed.
XX
XX Sequence 220 AA;
SQ
Query Match 12.6%; Score 136; DB 13; Length 220;
Best Local Similarity 24.6%; Pred. No. 2.3e-07;
Matches 42; Conservative 31; Mismatches 76; Indels 22; Gaps 7;
QY 30 MFIHNGVQILCKYPD--IVQEFKMLKGGQILCDLTKRSGN--TVSIRSLKRFCH 84
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 28 mlvaydnavnlsckysynlfrefraihkgldasavevcvnygsqlyysktgfncd 87
QY 85 SOLSNNSVSFFLYNLIDSHANYFCNLSIFDPPFP--KVTLTGGLHYESQLC----- 136
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 88 gklgnesvtlylqnlvnyqtdlyfcklevmypypldneksngtlhvkghkhlcpstlfp 147
QY 137 -COLKFWLPICACAFVVC---ILGCLILCWLTKKRYSSVHDPNGEYFM 182
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 148 gpskpfwlvvvgvylacysllvtvaflifwvrskr-slllh---sdyymm 194
Search completed: May 30, 2001, 16:49:46
Job time: 43 sec

```

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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:03 ; Search time 14.16 Seconds

(without alignments)
960.956 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 1078

Sequence: 1 MMSGIMYFFLFCIRIKVLTG.....YMFMAVNTAKSRLLDVTLL 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

PIR.67:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------|--------------------|
| 1 | 1067.5 | 99.0 | 199 | S78540 | Inducible T-cell c |
| 2 | 695.5 | 64.5 | 200 | JC7397 | activation-inducib |
| 3 | 690.5 | 64.1 | 216 | JC7396 | T-cell surface gly |
| 4 | 157.5 | 14.6 | 218 | S24413 | CD28 precursor - r |
| 5 | 147 | 13.6 | 221 | I46689 | T-cell surface gly |
| 6 | 141.5 | 13.1 | 218 | A43523 | cell surface gly |
| 7 | 138 | 12.8 | 173 | I46157 | T-cell surface gly |
| 8 | 136 | 12.6 | 220 | RMH028 | cell surface gly |
| 9 | 105.5 | 9.8 | 221 | S25168 | CH28 protein - ch |
| 10 | 93 | 8.6 | 223 | A29063 | hypothetical prote |
| 11 | 86 | 8.0 | 223 | T18986 | cytotoxic T-lympho |
| 12 | 86 | 8.0 | 383 | T21946 | hypothetical prote |
| 13 | 86 | 8.0 | 635 | JC5886 | Killer cell inhibi |
| 14 | 85.5 | 7.9 | 223 | T09536 | cytotoxic T-lympho |
| 15 | 83.5 | 7.7 | 285 | D69440 | conserved hypotet |
| 16 | 83 | 7.7 | 186 | S08614 | cytotoxic T-lympho |
| 17 | 82.5 | 7.7 | 248 | I0084L | probable glycopro |
| 18 | 81.5 | 7.6 | 330 | A40071 | Fc gamma (IgG) rec |
| 19 | 81.5 | 7.6 | 330 | I49660 | Fc gamma (IgG) rec |
| 20 | 81.5 | 7.6 | 363 | T32479 | hypothetical prote |
| 21 | 81.5 | 7.6 | 1584 | S57161 | hypothetical prote |
| 22 | 81 | 7.5 | 276 | S20690 | 31.6k hypothetical |
| 23 | 81 | 7.5 | 302 | I49660 | secretory compleme |
| 24 | 81 | 7.5 | 360 | I49660 | membrane bound com |
| 25 | 79.5 | 7.4 | 283 | JC5886 | Fc gamma (IgG) rec |
| 26 | 79.5 | 7.4 | 680 | JC5886 | Killer cell inhibi |
| 27 | 78.5 | 7.3 | 231 | T23136 | hypothetical prote |
| 28 | 78 | 7.2 | 235 | I50610 | T-cell surface gly |
| 29 | 77.5 | 7.2 | 220 | A48581 | 37k proline-rich s |

| | | | | | | |
|----|------|-----|------|---|--------|--------------------|
| 30 | 77.5 | 7.2 | 546 | 2 | S52053 | cytochrome-c oxida |
| 31 | 77 | 7.1 | 1070 | 2 | JC4593 | protein-tyrosine k |
| 32 | 76 | 7.1 | 301 | 2 | I54209 | hypothetical prote |
| 33 | 76 | 7.1 | 323 | 2 | S06946 | Fc gamma (IgG) rec |
| 34 | 75.5 | 7.0 | 261 | 2 | S29360 | Fc gamma (IgG) rec |
| 35 | 75.5 | 7.0 | 277 | 2 | T21330 | hypothetical prote |
| 36 | 75.5 | 7.0 | 1132 | 1 | OSBP | host specificity p |
| 37 | 75.5 | 7.0 | 2135 | 2 | T14602 | variant-specific s |
| 38 | 74.5 | 6.9 | 763 | 2 | S17998 | gene COX1 intron 4 |
| 39 | 74 | 6.9 | 223 | 2 | I46696 | CTLA-4 precursor - |
| 40 | 74 | 6.9 | 258 | 2 | E71646 | hypothetical prote |
| 41 | 74 | 6.9 | 496 | 2 | JH0165 | glycine receptor b |
| 42 | 74 | 6.9 | 496 | 2 | S46459 | glycine receptor b |
| 43 | 74 | 6.9 | 497 | 2 | G02031 | glycine receptor b |
| 44 | 73.5 | 6.8 | 275 | 2 | S61179 | probable membrane |
| 45 | 73.5 | 6.8 | 322 | 2 | I48207 | corticotropin-rele |

ALIGNMENTS

| | | |
|---|--------|---|
| RESULT 1 | 578540 | Inducible T-cell co-stimulator ICOS precursor - human |
| C:Species: Homo sapiens (man) | | |
| C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 07-May-1999 | | |
| C:Accession: S78540; S78748; S78749 | | |
| R:Kroczek, R. | | |
| Submitted to the Protein Sequence Database, June 1998 | | |
| A:Reference number: S78540 | | |
| A:Accession: S78540 | | |
| A:Molecule type: mRNA | | |
| A:Residues: 1-199 <KRO> | | |
| A:Experimental source: cell line MOLT-4V | | |
| R:Hutloff, A.; Dietrich, A.M.; Beier, K.C.; Eljaschewitsch, B.; Kraft, R.; Anagnostop | | |
| Nature 397, 263-266, 1999 | | |
| A:Title: ICOS is an inducible T-cell co-stimulator structurally and functionally rela | | |
| A:Reference number: S78748; MUID:99127892 | | |
| A:Accession: S78748 | | |
| A:Molecule type: mRNA | | |
| A:Residues: 1-199 <HUT1> | | |
| A:Experimental source: cell line MOLT-4V | | |
| A:Accession: S78749 | | |
| A:Molecule type: Protein | | |
| A:Residues: 'X', 193-198 <HUT2> | | |
| A:Experimental source: cell line MOLT-4V | | |
| C:Complex: homodimer | | |
| C:Superfamily: immunoglobulin homology | | |
| C:Keywords: dimer; glycoprotein; T-cell; transmembrane protein | | |
| F:1-19/Domain: (or 1-20) signal sequence #status predicted <SIG> | | |
| F:20-199/Product: (or 21-199) Inducible costimulator ICOS #status predicted <MAT> | | |
| F:21-136/Domain: extracellular #status predicted <EXT> | | |
| F:26-132/Domain: immunoglobulin homology <IMM> | | |
| F:139-164/Domain: transmembrane #status predicted <TMN> | | |
| F:165-199/Domain: intracellular #status predicted <INT> | | |
| F:23,89,110/Binding site: carbohydrate (Asn) (covalent) #status predicted | | |
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| Best Local Similarity | 99.5% | Pred. No. 8.5e-97; |
| Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1; | | |
| Db | 1 | MMSGIMYFFLFCIRIKVLTGELNSANYEMFTHNGVQILCKYPDIYQGRKMLKGGQ 60 |
| Qy | 1 | MMSGIMYFFLFCIRIKVLTGELNSANYEMFTHNGVQILCKYPDIYQGRKMLKGGQ 60 |
| Db | 1 | MMSGIMYFFLFCIRIKVLTGELNSANYEMFTHNGVQILCKYPDIYQGRKMLKGGQ 60 |
| Qy | 61 | ILCDLTKRGSGNYSISLKFCHSOLSNNSVSFFLYMLDHSNANYFCNLSIDPPPFK 120 |
| Db | 61 | ILCDLTKRGSGNYSISLKFCHSOLSNNSVSFFLYMLDHSNANYFCNLSIDPPPFK 120 |
| Qy | 121 | VTLNGGYLHIESOLCCOLKFWLPICGAAV-VCTILGICILCWLTKKRYSSVHDPPNGEY 179 |
| Db | 121 | VTLNGGYLHIESOLCCOLKFWLPICGAAV-VCTILGICILCWLTKKRYSSVHDPPNGEY 180 |

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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:03 ; Search time 13.01 Seconds
(without alignments)
292.371 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 1078
Sequence: 1 MMSGWTFYFLFCLRIKVLG.....YMFRAVNTAKKSLIDVTL 198

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Seatched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 159.5 | 14.8 | 218 | 3 | US-08-228-208A-20 |
| 2 | 143 | 13.3 | 225 | 1 | US-08-505-058-4 |
| 3 | 143 | 13.3 | 225 | 2 | US-08-459-818-24 |
| 4 | 143 | 13.3 | 225 | 2 | US-08-889-666-24 |
| 5 | 143 | 13.3 | 225 | 2 | US-08-465-078-24 |
| 6 | 143 | 13.3 | 225 | 2 | US-08-725-776-24 |
| 7 | 143 | 13.3 | 225 | 2 | US-08-488-062-24 |
| 8 | 135.5 | 12.6 | 218 | 3 | US-08-228-208A-19 |
| 9 | 130 | 12.1 | 220 | 1 | US-08-228-208A-21 |
| 10 | 129.5 | 12.0 | 225 | 1 | US-08-505-058-3 |
| 11 | 128.5 | 12.0 | 225 | 2 | US-08-459-818-23 |
| 12 | 128.5 | 12.0 | 225 | 2 | US-08-889-666-23 |
| 13 | 128.5 | 12.0 | 225 | 2 | US-08-465-078-23 |
| 14 | 129.5 | 12.0 | 225 | 2 | US-08-725-776-23 |
| 15 | 129.5 | 12.0 | 225 | 2 | US-08-488-062-23 |
| 16 | 121.5 | 11.3 | 223 | 1 | US-08-505-058-5 |
| 17 | 121.5 | 11.3 | 223 | 2 | US-08-459-818-25 |
| 18 | 121.5 | 11.3 | 223 | 2 | US-08-889-666-25 |
| 19 | 121.5 | 11.3 | 223 | 2 | US-08-465-078-25 |
| 20 | 121.5 | 11.3 | 223 | 2 | US-08-725-776-25 |
| 21 | 121.5 | 11.3 | 223 | 2 | US-08-488-062-25 |
| 22 | 120.5 | 11.2 | 367 | 3 | US-08-630-172-19 |
| 23 | 119.5 | 11.1 | 134 | 3 | US-08-630-172-3 |
| 24 | 97.5 | 9.0 | 221 | 3 | US-08-228-208A-22 |
| 25 | 89.5 | 8.3 | 117 | 3 | US-08-529-878B-39 |
| 26 | 84.5 | 7.8 | 226 | 1 | US-08-505-058-6 |
| 27 | 84.5 | 7.8 | 226 | 2 | US-08-459-818-26 |

| | | | | | | |
|----|------|-----|-----|---|--------------------|-------------------|
| 28 | 84.5 | 7.8 | 226 | 2 | US-08-889-666-26 | Sequence 26, Appl |
| 29 | 84.5 | 7.8 | 226 | 2 | US-08-465-078-26 | Sequence 26, Appl |
| 30 | 84.5 | 7.8 | 226 | 2 | US-08-725-776-26 | Sequence 26, Appl |
| 31 | 84.5 | 7.8 | 226 | 2 | US-08-488-062-26 | Sequence 17, Appl |
| 32 | 83.5 | 7.7 | 223 | 3 | US-08-228-208A-17 | Sequence 17, Appl |
| 33 | 81.5 | 7.6 | 330 | 2 | US-08-333-562A-81 | Sequence 81, Appl |
| 34 | 81.5 | 7.6 | 330 | 2 | US-08-333-562A-134 | Sequence 134, App |
| 35 | 81 | 7.5 | 187 | 1 | US-08-067-684-14 | Sequence 14, Appl |
| 36 | 81 | 7.5 | 187 | 1 | US-08-008-898-14 | Sequence 14, Appl |
| 37 | 81 | 7.5 | 187 | 2 | US-08-459-818-14 | Sequence 14, Appl |
| 38 | 81 | 7.5 | 187 | 2 | US-08-889-666-14 | Sequence 14, Appl |
| 39 | 81 | 7.5 | 187 | 2 | US-08-465-078-14 | Sequence 14, Appl |
| 40 | 81 | 7.5 | 187 | 2 | US-08-725-776-14 | Sequence 14, Appl |
| 41 | 81 | 7.5 | 187 | 2 | US-08-488-062-14 | Sequence 14, Appl |
| 42 | 81 | 7.5 | 187 | 3 | US-08-228-208A-14 | Sequence 14, Appl |
| 43 | 81 | 7.5 | 187 | 3 | PCT-US95-06726-36 | Sequence 36, Appl |
| 44 | 80.5 | 7.5 | 234 | 1 | US-08-505-058-1 | Sequence 1, Appl |
| 45 | 80.5 | 7.5 | 234 | 2 | US-08-459-818-21 | Sequence 21, Appl |

ALIGNMENTS

RESULT 1
; Sequence 20, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Mith K.
; APPLICANT: Brady, William M.
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD2819 HYBRID FUSION
; TITLE OF INVENTION: PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-228-208A-20

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Query Match 14.8% Score 159.5 DB 3 Length 218:
Best Local Similarity 25.8% Pred No.5.4e-11
Matches 40; Conservative 30; Mismatches 66; Indels 19; Gaps 7.

OY 30 MEFINGVQVILCKKPPD--IVQAFKMLKLGQIICDLKRTKSGNTVSIKSLK-----F 82
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 29 LLVYDNNETSLSCRSYNNLAKERFASLYKG--VMSDVEVCVGNNGFTYQQPFRRVWGFN 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 83 CHSGLSNNSVSFFLYNLDSHANYIFCNLSIPDPPE--KVTLLTGAYLHYESQLC----- 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 87 CDGNDNETVETFRLLNLLVNNHFDIFYCKIEVAYPPPYLDNEKSNGTIIHKKEKHLCHAQT 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY 137 GQLKFWLPICGAAFVVC--ILGCIILIC--WLTKKK 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 147 SPKLEWPLVVVAVAGVLLCYGLTYTLVLCITITWNSRK 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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1      RESULT      2
2      US-08-505-058-4
3      Sequence 4, Application US/08505058
4      Invent No. 5773253
5      GENERAL INFORMATION:
6      APPLICANT: Linsley, Peter S.
7      APPLICANT: Ledbetter, Jeffrey A.
8      APPLICANT: Peach, Robert
9      TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
10     NUMBER OF SEQUENCES: 13
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Merchant & Gould
13     STREET: 11150 Santa Monica Blvd., Suite 400
14     CITY: Los Angeles
15     STATE: California
16     COUNTRY: USA
17     ZIP: 90025
18     COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: PatentIn Release #1.0, Version #1.30
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/505,058
25     FILING DATE:
26     CLASSIFICATION: 435
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER: 08/228,208
29     FILING DATE: 15-APR-1994
30     ATTORNEY/AGENT INFORMATION:
31     NAME: Adliano, Sarah B.
32     REGISTRATION NUMBER: 34,470
33     REFERENCE/DOCKET NUMBER: 30436.300S11
34     TELECOMMUNICATION INFORMATION:
35     TELEPHONE: 310-445-1140
36     TELEFAX: 310-445-9031
37     INFORMATION FOR SEQ ID NO: 4:
38     SEQUENCE CHARACTERISTICS:
39     LENGTH: 225 amino acids
40     TYPE: amino acid
41     STRANDEDNESS:
42     TOPOLOGY: linear
43     MOLECULE TYPE: protein
44     US-08-505-058-4

```

```

Query Match      13.3%   Score 143:   DB 1:   Length 225;
Best Local Similarity 25.6%   Pred. No. 5e-09;
Matches 41; Conservative 30; Mismatches 65; Indels 24; Gaps 9

Oy - 30 MEIFINGVQIIL-CRYPD--IVQQRMLKKGQIICLDLTKT-KSGNGTVSISLK-----81
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  , 30 LLYVDNNEVSLSCRYSYNLAKERRASLYLK--VNSVDYEVCGVGNITVQDPFPPNNG 87
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Oy      82 -FCHSOLSNNSVSFFLYLNDHSHANYECNLSIDPDPF--KVLITGYGLYIESOLC-- 136
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      88 FNCOSGPNFNEVETFRMLNLDVNHNDIYFCRLEWYPPPIIDNEKSNSTIIHIEKHCHHA 147

Oy      137 -----COLFWPLPGICAAFYVC--ILGCILIC--WLTKKK 167
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      148 XXXXOTSPKLEPPLVAVAGVGLTCTGELTTLVTLCIIWTNSRR 187

```

```

1      RESULT 3
2      US-08-459-818-24
3      : Sequence 24, Application US/08459818
4      : Patent No. 5851795
5      : GENERAL INFORMATION:
6      : APPLICANT: Linsley, Peter S.
7      : APPLICANT: Ledbetter, Jeffrey A.
8      : APPLICANT: Damle, Nitin K.
9      : APPLICANT: Brady, William
10     : TITLE OF INVENTION: CTL44 Receptor and Uses Thereof
11     : NUMBER OF SEQUENCES: 27
12     : CORRESPONDENCE ADDRESS:
13     : ADDRESSEE: Merchant & Gould
14     : STREET: 1150 Santa Monica Blvd., Suite 400
15     : CITY: Los Angeles
16     : STATE: California
17     : COUNTRY: USA
18     : ZIP: 90025
19     : COMPUTER READABLE FORM:
20     : MEDIUM TYPE: Floppy disk
21     : COMPUTER: IBM PC compatible
22     : OPERATING SYSTEM: PC-DOS/MS-DOS
23     : SOFTWARE: Fastseq 2.0
24     : CURRENT APPLICATION DATA:
25     : APPLICATION NUMBER: US/08/459,818
26     : FILING DATE: 02-JUN-1995
27     : CLASSIFICATION: 435
28     : ATTORNEY/AGENT INFORMATION:
29     : NAME: Adriano, Sarah B.
30     : REGISTRATION NUMBER: 34,470
31     : REFERENCE/DOCKET NUMBER: 30436.35US02
32     : TELECOMMUNICATION INFORMATION:
33     : TELEPHONE: 310-445-1140
34     : TELEFAX: 310-445-9031
35     : INFORMATION FOR SEQ ID NO: 24:
36     : SEQUENCE CHARACTERISTICS:
37     : LENGTH: 225 amino acids
38     : TYPE: amino acid
39     : STRANDEDNESS:
40     : TOPOLOGY: linear
41     : MOLECULE TYPE: protein
42     : US-08-459-818-24

```

| | | | | |
|--------------------------|-------------|--|-------|-----------------------------------|
| Query Match | 13.3% | Score 143; | DB 2; | length 225; |
| Best Local Similarity | 25.6% | Pred. No. 5e-09; | | |
| Matches | 41; | Conservative | 30; | Mismatches 65; Indels 24; Gaps 9; |
| Oy | 30 | MEIFINGGVQII-CRYPD--IVQOFKMOGLKGQILCDLTKT-KSGSGTVSIKSLK---- | 81 | |
| Db | 30 | LLVYDNNNEVXSLSCRYSYNLLAKERASLYKK--VNSDVXEVCVGNGETPYOPFRPNVG | 87 | |
| Oy | 82 | -FCHSOLSNNSVSFFLYLNDHSHAVYFCNLSIFDPFP--KVLTGTGGLHIYESOLC-- | 136 | |
| Db | 88 | FNCDGNFENETVETFLMNDVNHDTDYFCFKIEVMPRPPLDNEKNSGFTIIHIKEKHLCHA | 147 | |
| Oy | 137 | -----COLKFWLPIGCAAFVVC--TLGLGILC--WLTKKK | 167 | |
| Db | 148 | XXXQTSRKLFMPLYVAVGVLCTGGLLYVTVLTCTITNSRR | 187 | |
| RESULT | 4 | | | |
| US-08-889-666-24 | | | | |
| Sequence 24, Application | US/08889666 | | | |

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:23 ; Search time 22.68 Seconds

(Without alignments)
1023.244 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 1078
Sequence: 1 MMSGLMWFFLFCLRIKVLG.....YMFRAVNTAKSRIDVTL 198

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL.15:*
1: sp_bacteria:*
2: sp_fungi:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rudent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1067.5 | 99.0 | 199 | 4 | O9Y6W8 |
| 2 | 727 | 67.4 | 200 | 11 | O9WVS0 |
| 3 | 723.5 | 67.1 | 200 | 11 | O9JL17 |
| 4 | 695.5 | 64.5 | 200 | 11 | O9R1T7 |
| 5 | 690.5 | 64.1 | 216 | 11 | O9WVS9 |
| 6 | 142 | 13.2 | 221 | 11 | O9JLV4 |
| 7 | 141 | 13.1 | 221 | 6 | O02757 |
| 8 | 141 | 13.1 | 221 | 6 | O9N214 |
| 9 | 139 | 12.9 | 221 | 6 | O9N0N8 |
| 10 | 138.5 | 12.8 | 219 | 6 | O97630 |
| 11 | 138 | 12.8 | 173 | 6 | O28289 |
| 12 | 93 | 8.6 | 988 | 5 | O17710 |
| 13 | 86 | 8.0 | 485 | 5 | O20139 |
| 14 | 86 | 8.0 | 635 | 11 | O55002 |
| 15 | 86 | 8.0 | 663 | 11 | O70434 |
| 16 | 84 | 7.8 | 223 | 11 | O9QZ27 |
| 17 | 84 | 7.8 | 419 | 13 | O9IA91 |
| 18 | 83.5 | 7.7 | 285 | 1 | O28747 |
| 19 | 83 | 7.7 | 209 | 4 | O9NYK4 |

| | | | | | | |
|----|------|-----|-----|----|--------|--------------------|
| 20 | 83 | 7.7 | 223 | 11 | O9JLV3 | O9JLV3 marmota mon |
| 21 | 82 | 7.6 | 296 | 14 | O73315 | O73315 human immun |
| 22 | 81.5 | 7.6 | 223 | 11 | O62859 | O62859 ratius norv |
| 23 | 81.5 | 7.6 | 563 | 5 | O17395 | O17395 caenorhabdi |
| 24 | 81 | 7.5 | 276 | 14 | O98822 | O98822 human adeno |
| 25 | 81 | 7.5 | 276 | 14 | O64861 | O64861 human adeno |
| 26 | 80.5 | 7.5 | 321 | 4 | O9UGF6 | O9UGF6 homo sapien |
| 27 | 80 | 7.4 | 761 | 11 | O9R1C0 | O9R1C0 mus musculu |
| 28 | 79.5 | 7.4 | 680 | 11 | O55001 | O55001 mus musculu |
| 29 | 78.5 | 7.3 | 231 | 5 | O45668 | O45668 caenorhabdi |
| 30 | 78.5 | 7.3 | 539 | 14 | P88842 | P88842 avian infec |
| 31 | 78 | 7.2 | 235 | 13 | O90770 | O90770 gallus gall |
| 32 | 78 | 7.2 | 269 | 4 | O95297 | O95297 homo sapien |
| 33 | 77.5 | 7.2 | 546 | 8 | O35989 | O35989 trypanoplas |
| 34 | 77 | 7.1 | 415 | 10 | O9LW05 | O9LW05 arabidopsis |
| 35 | 76.5 | 7.1 | 539 | 14 | P88839 | P88839 avian infec |
| 36 | 76.5 | 7.1 | 539 | 14 | P88840 | P88840 avian infec |
| 37 | 76.5 | 7.1 | 539 | 14 | P88843 | P88843 avian infec |
| 38 | 76.5 | 7.1 | 619 | 10 | O9XG01 | O9XG01 sorghum bic |
| 39 | 76.5 | 7.1 | 863 | 10 | O9M0D8 | O9M0D8 arabidopsis |
| 40 | 76 | 7.1 | 174 | 11 | O9Z1A7 | O9Z1A7 ratius norv |
| 41 | 76 | 7.1 | 192 | 14 | O11432 | O11432 avian adeno |
| 42 | 76 | 7.1 | 448 | 11 | O88597 | O88597 mus musculu |
| 43 | 76 | 7.1 | 450 | 4 | O75595 | O75595 homo sapien |
| 44 | 76 | 7.1 | 450 | 4 | O9UN48 | O9UN48 homo sapien |
| 45 | 76 | 7.1 | 948 | 5 | O9YD07 | O9YD07 drosophila |

ALIGNMENTS

RESULT 1
ID O9Y6W8 PRELIMINARY; PRT; 199 AA.
AC O9Y6W8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DF 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE AILIM
DE PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
transmission";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB02135; BAA82129.1; -;
KW Signal.
FT SIGNAL.
SQ SEQUENCE 199 AA; 22624 MW; 21AEC741C9BDC9FC CRC64;

Query Match 99.0%; Score 1067.5; DB 4; Length 199;
Best Local Similarity 99.5%; Pred. No. 7.6e-106;
Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 MMSGLMWFFLFCLRIKVLGGEINGSANYEMFTEHNGVOILLKYPDIYVOFMOLLKGGQ 60
DB 1 MMSGLMWFFLFCLRIKVLGGEINGSANYEMFTEHNGVOILLKYPDIYVOFMOLLKGGQ 60
OY 61 IICDLTKTKGSGNTVSIRKSLKCHSOLSNNSVSFFELYNIDSHANYFCNLSIFPPPPK 120
DB 61 IICDLTKTKGSGNTVSIRKSLKCHSOLSNNSVSFFELYNIDSHANYFCNLSIFPPPPK 120
OY 121 VLTGGLYHIVYSOLCCQQLKFWLPITGCAAF-VVCIIGCTLICLWLTKKYSVHPDNGEY 179
DB 121 VLTGGLYHIVYSOLCCQQLKFWLPITGCAAFVVVCIIGCTLICLWLTKKYSVHPDNGEY 180

QY 180 MEMRAVNTAKSRRLDVT 198
 DB 181 MEMRAVNTAKSRRLDVT 199

RESULT 2

Q9WVSO PRELIMINARY; PRT; 200 AA.
 AC Q9WVSO; 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATOR MOLECULE ALLIM
 DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).
 GN CCLP OR ICOS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RA Tezuka K., Tamatani T.;
 RL "Cell surface molecule mediating cell adhesion and signal
 transmission.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=SPLEEN;
 RA Wu D., Giannoni M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,
 RA Mattis L.A., Rother R.P.;
 RL "CCLP, A novel molecule that regulates T cell activation."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=SPLEEN;
 RA Mages H.W., Hultlof A., Heuck C., Buchner K., Himmelbauer H.,
 RA Oliveri F., Kroczeck R.A.;
 RL "Molecular cloning and characterization of murine ICOS and
 RT Identification of B7h as ICOS ligand."
 RL Eur. J. Immunol. 30:1040-1047(2000).
 DR EMBL: AB023132; BAA82126.1; -
 DR EMBL: AF257230; AAF70099.1; -
 DR EMBL: AJ250559; CAB71153.1; -
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 200 AA; 22690 MW; 9B2278EACAB1D847 CRC64;

Query Match 67.4%; Score 727; DB 11; Length 200;
 Best Local Similarity 69.3%; Pred. No. 1.3e-69;

Matches 138; Conservative 20; Mismatches 39; Indels 2; Gaps 2;

QY 1 MKSGLMFLEFLIKVLTGINSANTEMIFHNGVQILCKPDYQKMLLKGQ 60
 DB 1 MKPEYCHVFECFIRLITGINSADHRMFSFHNGVQISCKPEYQKMLLFRERE 60
 QY 61 ILCDLTKSGNVTISIKSLKFCQSOLSNNSVFLNLDHSHANYFCNLSTDPPEPK 120
 DB 61 VLCELTTKSGNAVSIKKNMLCLYHLSNNSVSFFLNPPDSQSYFCSLSTDPPEPK 120
 QY 121 V-ITLGGYLIHYESQLCCQLKFWLPICCAAFVVCIL-GCILICMLTKKYSVHPDNGE 178
 DB 121 ERNLGSGYLHYESQLCCQLKFWLPVGCACAFVAVVLLFGCILIIIFSKKYGSSVHPDNGE 180
 QY 179 YMFRAVNTAKSRRLDVT 197
 DB 181 YMFMAAVNTKSRRLAGVT 199

RESULT 3
 Q9JUL17 PRELIMINARY; PRT; 200 AA.
 DB Q9JUL17

AC Q9JUL17;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATOR MOLECULE ALLIM
 DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).
 GN CCLP OR ICOS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS; INTRA-EPITHELIUM;
 RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
 RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Taturt-Bladt A.,
 RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,
 RA Hul A., McCabe S.M., Scully S., Shalke C.L., Van G., Mak T.W.,
 RA Senaldi G.;
 RL "T-cell co-stimulation through B7RP-1 and ICOS."
 RL Nature 0:0-0(2000).
 DR EMBL: AF216748; AAF45150.1; -
 FT NON_TER 200
 SQ SEQUENCE 200 AA; 22709 MW; 87D97FDDC44ADCA7 CRC64;

Query Match 67.1%; Score 723.5; DB 11; Length 200;
 Best Local Similarity 70.4%; Pred. No. 3.1e-69;

Matches 138; Conservative 19; Mismatches 34; Indels 5; Gaps 3;

QY 7 YF--FLFCURIKVLTGINSANTEMIFHNGVQILCKPDYQKMLLKGQILC 63
 DB 4 YFCRVFVFCFIRLITGINSADHRMFSFHNGVQISCKPEYQKMLLFREREYLC 63
 QY 64 DLTKSGNVTISIKSLKFCQSOLSNNSVFLNLDHSHANYFCNLSTDPPEPKV-T 122
 DB 64 ELTKSGNAVSIKKNMLCLYHLSNNSVSFFLNPPDSQSYFCSLSTDPPEPKERN 123
 QY 123 LTGGYLIHYESQLCCQLKFWLPICCAAFVVCIL-GCILICMLTKKYSVHPDNGEYMF 181
 DB 124 LSGGYLIHYESQLCCQLKFWLPVGCACAFVAVVLLFGCILIIIFSKKYGSSVHPDNGEYMF 183
 QY 182 MRAVNTAKSRRLDVT 197
 DB 184 MAAVNTKSRRLAGVT 199

RESULT 4

Q9R1T7 PRELIMINARY; PRT; 200 AA.
 AC Q9R1T7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATOR MOLECULE ALLIM
 DE PRECURSOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tezuka K., Tamatani T.;
 RL "Cell surface molecule mediating cell adhesion and signal
 transmission."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB023134; BAA82128.1; -
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 200 AA; 22529 MW; 0A74C35581F129D4 CRC64;

Query Match 64.5%; Score 695.5; DB 11; Length 200;
 Best Local Similarity 68.4%; Pred. No. 2.9e-66;
 Matches 134; Conservative 17; Mismatches 40; Indels 5; Gaps 3;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2001, 16:49:48 ; Search time 9.54 Seconds

(without alignments)
710.963 Million cell updates/sec

Title: US-09-509-283-2

Sequence: 1 MMSGLMYFLFLCLRIKVLFG.....YMFMRVNTAKSKRLDVTLL 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 155.5 | 14.4 | 218 | 1 | CD28_RAT |
| 2 | 147 | 13.6 | 221 | 1 | P31042 rattus norv |
| 3 | 141.5 | 13.1 | 218 | 1 | P42069 oryctolagus |
| 4 | 136 | 12.6 | 220 | 1 | CD28_MOUSE |
| 5 | 134.5 | 12.5 | 219 | 1 | CD28_HUMAN |
| 6 | 105.5 | 9.8 | 221 | 1 | CD28_BOVIN |
| 7 | 86 | 8.0 | 223 | 1 | CD28_CHICK |
| 8 | 85.5 | 7.9 | 223 | 1 | CD28_MOUSE |
| 9 | 82.5 | 7.7 | 248 | 1 | CD28_HUMAN |
| 10 | 81.5 | 7.6 | 330 | 1 | CD28_MOUSE |
| 11 | 81.5 | 7.6 | 330 | 1 | CD28_MOUSE |
| 12 | 81 | 7.5 | 1584 | 1 | CD28_MOUSE |
| 13 | 77.5 | 7.2 | 324 | 1 | CD28_MOUSE |
| 14 | 77 | 7.1 | 1070 | 1 | CD28_MOUSE |
| 15 | 76 | 7.1 | 448 | 1 | CD28_MOUSE |
| 16 | 76 | 7.1 | 448 | 1 | CD28_MOUSE |
| 17 | 76 | 7.1 | 448 | 1 | CD28_MOUSE |
| 18 | 75.5 | 7.0 | 261 | 1 | CD28_MOUSE |
| 19 | 75.5 | 7.0 | 261 | 1 | CD28_MOUSE |
| 20 | 75.5 | 7.0 | 261 | 1 | CD28_MOUSE |
| 21 | 74 | 6.9 | 1132 | 1 | CD28_MOUSE |
| 22 | 74 | 6.9 | 344 | 1 | CD28_MOUSE |
| 23 | 74 | 6.9 | 496 | 1 | CD28_MOUSE |
| 24 | 74 | 6.9 | 496 | 1 | CD28_MOUSE |
| 25 | 74 | 6.9 | 496 | 1 | CD28_MOUSE |
| 26 | 73.5 | 6.8 | 275 | 1 | CD28_MOUSE |
| 27 | 73.5 | 6.8 | 275 | 1 | CD28_MOUSE |
| 28 | 73.5 | 6.8 | 275 | 1 | CD28_MOUSE |
| 29 | 73.5 | 6.8 | 275 | 1 | CD28_MOUSE |
| 30 | 73 | 6.8 | 1162 | 1 | CD28_MOUSE |
| 31 | 72 | 6.7 | 569 | 1 | CD28_MOUSE |
| 32 | 71.5 | 6.6 | 317 | 1 | CD28_MOUSE |
| 33 | 71.5 | 6.6 | 1154 | 1 | CD28_MOUSE |

ALIGNMENTS

| | | | | | |
|----|------|-----|------|---|------------|
| 34 | 71.5 | 6.6 | 1163 | 1 | WGL2_IBVD |
| 35 | 71.5 | 6.6 | 2768 | 1 | THYG_HUMAN |
| 36 | 71 | 6.6 | 329 | 1 | CD86_HUMAN |
| 37 | 71 | 6.6 | 372 | 1 | CD86_HUMAN |
| 38 | 71 | 6.6 | 524 | 1 | CD86_HUMAN |
| 39 | 71 | 6.6 | 634 | 1 | CD86_HUMAN |
| 40 | 71 | 6.6 | 1051 | 1 | CD86_HUMAN |
| 41 | 70.5 | 6.5 | 322 | 1 | CD86_HUMAN |
| 42 | 70.5 | 6.5 | 466 | 1 | CD86_HUMAN |
| 43 | 70.5 | 6.5 | 520 | 1 | CD86_HUMAN |
| 44 | 70.5 | 6.5 | 550 | 1 | CD86_HUMAN |
| 45 | 70.5 | 6.5 | 561 | 1 | CD86_HUMAN |

RESULT 1
ID CD28_RAT STANDARD: PRT: 218 AA.

AC P31042:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE T-CELL-SPECIFIC SURFACE GLYCOPROTEIN CD28 PRECURSOR.
GN CD28.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP STRAIN=DA; TISSUE=Lymphoid;
RC MEDLINE=92104640; PubMed=1309509;
RA Clark G.J., Dailman M.J.;
RT Identification of a cDNA encoding the rat CD28 homologue.*;
RL Immunogenetics 35:54-57(1992).

CC -1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1 AND B7-2 (B70).
CC -1- SUBUNIT: HOMODIMER, LINKED BY A DISULFIDE BOND.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. STRONGEST SIMILARITY TO CTLA-4.

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DR EMBL: X55288; CAA39003.1; -;
DR PIR: S38722; S38722.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane.

| | | | |
|-------------|---------|-----------|--------------------------------------|
| FT SIGNAL | 1 | 19 | BY SIMILARITY. |
| FT CHAIN | 20 | 218 | T-CELL-SPECIFIC SURFACE GLYCOPROTEIN |
| FT DOMAIN | 20 | 150 | EXTRACELLULAR (POTENTIAL). |
| FT TRANSMEM | 151 | 177 | POTENTIAL. |
| FT DOMAIN | 178 | 218 | CYTOPLASMIC (POTENTIAL). |
| FT DOMAIN | 29 | 138 | IG-LIKE V-TYPE DOMAIN. |
| FT CARBOHYD | 72 | 72 | N-LINKED (GLCNAc. . .) (POTENTIAL). |
| FT CARBOHYD | 93 | 93 | N-LINKED (GLCNAc. . .) (POTENTIAL). |
| FT CARBOHYD | 106 | 106 | N-LINKED (GLCNAc. . .) (POTENTIAL). |
| FT CARBOHYD | 130 | 130 | N-LINKED (GLCNAc. . .) (POTENTIAL). |
| SEQ | 218 AA: | 25170 MW; | 2E151C8F324C0B6E CXC64; |

Query Match 14.4%; Score 155.5; DB 1; Length 218;
Best Local Similarity 25.8%; Pred. No. 3.1e-08;
Matches 40; Conservative 29; Mismatches 67; Indels 19; Gaps 7;

PR 26-FEB-1999; 99US-0258670.
 PR 06-OCT-1999; 99US-0413136.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;
 XX WPI: 2000-303619/26.
 DR N-PSDB; A09056.
 XX
 PT T helper (Th) 2 nucleic acids and encoded proteins, useful for the
 PT diagnosis and treatment of immune and respiratory disorders such as
 PT Crohn's diseases, arthritis, insulin dependent diabetes and
 PT autoimmunity
 XX
 PS Claim 16; Page 138-139; 159pp; English.
 XX
 CC This Th2-specific polypeptide, which has similarity to human CD28 and
 CC human CTLA-4 is encoded by human orthologue h1228.
 CC A novel method for modulating a Th2 response, an immune response, or
 CC suppressing airway inflammation or hyperresponsiveness in a mammal
 CC comprises administering a Th2-specific polypeptide of the invention, an
 CC antibody to such a polypeptide or allelic variants of the genes. The
 CC novel DNA and polypeptide sequences are useful for treatment and
 CC diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,
 CC arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
 CC dermatitis, psoriasis, graft rejection, graft versus host diseases,
 CC sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
 CC viral infections (including human immunodeficiency virus (HIV)),
 CC bacterial infections, bronchitis, cystic fibrosis, diphtheria,
 CC emphysema, pneumonia, and Legionnaires disease.
 CC
 SQ Sequence 198 AA;
 XX

Query Match 76.8%; Score 152; DB 21; Length 198;
 Best Local Similarity 100.0%; Pred. No. 3.5e-149;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKSGLMWFFLECLRIKIVLTGEINGSANYEMFIFHNGVQILCKYPIVQOFKQMLKGGQ 60
 |||||||
 DB 1 mksglwyfflfcrltkvltgelingsanyemflfmgvqllckypdivqfkmqllkxgq 60
 |||||||

OY 61 ILCDLTKGSGNTVSIRKSLKFCQSOLSNNSVSFFLYNLDSHANYEFCNLSTFDPPPFK 120
 |||||||
 DB 61 ilcdltksgnsvtsirsklfcqsolsnnsvsfflynlshanyyfcnlstfdppfk 120
 |||||||

OY 121 VTLLGYLHLYESQLCQCLKFWLPIGCAAFV 152
 |||||||
 DB 121 vtllgyllhlyesqlccqlkfwlpligcaafv 152
 |||||||

RESULT 2
 ID W75956
 W75956 standard; Protein: 199 AA.
 XX
 AC W75956;
 XX
 DT 11-DEC-1998 (first entry)
 XX
 DE Human cell surface protein #1.
 XX
 KW Human: cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 OS Homo sapiens.
 XX
 PN WO9838216-A1.
 XX
 PD 03-SEP-1998.
 XX
 PR 27-FEB-1998; 98WO-JP00837.
 PF

XX
 PR 26-FEB-1998; 98JP-0062217.
 PR 27-FEB-1997; 97JP-0062290.
 XX
 PA (NISB) JAPAN TOBACCO INC.
 XX
 PI Tamatani T, Tezuka K;
 XX WPI: 1998-481144/41.
 DR N-PSDB; V53198.
 XX
 PT Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of auto-immune and allergic disorders.
 XX
 PS Claim 2; Page 99-101; 149pp; Japanese.
 XX
 CC The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence RDPPEF in its extracellular region and the
 CC sequence YMFN in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 CC
 SQ Sequence 199 AA;
 XX

Query Match 76.8%; Score 152; DB 19; Length 199;
 Best Local Similarity 100.0%; Pred. No. 3.5e-149;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKSGLMWFFLECLRIKIVLTGEINGSANYEMFIFHNGVQILCKYPIVQOFKQMLKGGQ 60
 |||||||
 DB 1 mksglwyfflfcrltkvltgelingsanyemflfmgvqllckypdivqfkmqllkxgq 60
 |||||||

OY 61 ILCDLTKGSGNTVSIRKSLKFCQSOLSNNSVSFFLYNLDSHANYEFCNLSTFDPPPFK 120
 |||||||
 DB 61 ilcdltksgnsvtsirsklfcqsolsnnsvsfflynlshanyyfcnlstfdppfk 120
 |||||||

OY 121 VTLLGYLHLYESQLCQCLKFWLPIGCAAFV 152
 |||||||
 DB 121 vtllgyllhlyesqlccqlkfwlpligcaafv 152
 |||||||

RESULT 3
 ID W75957
 W75957 standard; Protein: 199 AA.
 XX
 AC W75957;
 XX
 DT 11-DEC-1998 (first entry)
 XX
 DE Human cell surface protein #2.
 XX
 KW Human: cell surface protein; thymocyte; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 OS Homo sapiens.
 XX
 PN WO9838216-A1.
 XX
 PD 03-SEP-1998.
 XX
 PR 27-FEB-1998; 98WO-JP00837.
 XX
 PR 26-FEB-1998; 98JP-0062217.
 PR 27-FEB-1997; 97JP-0062290.
 XX

PA (NISB) JAPAN TOBACCO INC.
 XX
 PI Tamatani T, Tezuka K;
 XX
 DR WPI: 1998-481144/41.
 DR N-PSDB: V53199.
 XX
 PT Cell surface molecule expressed in thymocytes and lymphocytes and -
 PT mediating signal transmission and cell adhesion, and antibodies to
 PT it useful in treatment of auto-immune and allergic disorders.
 XX
 PS Claim 9: Page 101-105; 149pp; Japanese.
 CC
 CC The present sequence represents a human cell surface protein which is
 CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
 CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
 CC antibodies recognising the cell surface protein. These antibodies also
 CC produce an increase in peripheral blood lymphocytes in the presence of
 CC an antibody recognising CD3 antigen. The cell surface protein contains
 CC the amino acid sequence FPPPPF in its extracellular region and the
 CC sequence YMFH in its intracellular region. The cell surface protein can
 CC be used in the prevention and treatment of autoimmune and allergic
 CC diseases, and in the diagnosis and investigation of such disorders.
 CC
 XX
 SQ Sequence 199 AA:
 Query Match 76.8%; Score 152; DB 19; Length 199;
 Best Local Similarity 100.0%; Pred. No. 3.5e-149;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMSGIWFPLFLRLIKVLTGEINGSANVEMFIFHNGVQIICKYPIYQOEFKMLIKGQ 60
 Db 1 mksglwyfflfcrlrlkvtlgeingsanvemifhngvqilckypdivqfkmqllksgq 60
 QY 61 IICDLTKTKGSGNTWSIKSLKFCCHSOLSNNSVSFFLYNIDSHANYFCNLSIFDPPPK 120
 Db 61 IICDLTKTKGSGNTWSIKSLKFCCHSOLSNNSVSFFLYNIDSHANYFCNLSIFDPPPK 120
 QY 121 VLTGGLHYEVSQCCOLKFWLPICGAFV 152
 Db 121 vltggylhyesqccqlkfwlpigcaafv 152
 RESULT 4
 26
 Y08026 standard; Protein: 199 AA.
 XX
 AC Y08026;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE Human activated T-lymphocyte protein 8F4.
 XX
 KW T-lymphocyte; human; 8F4; T cell co-stimulation; activated; CD4+; CD8+;
 KW anticancer; antiviral; anti-asthma; immunomodulator; proliferation;
 KW T cell activation; cytokine synthesis; regulatory element; B cell;
 KW T cell-dependent antibody production; treatment; prevention; cancer;
 KW autoimmune disease; transplant rejection; immune system regulation;
 KW disorder; acquired immune deficiency syndrome; AIDS; asthma.
 XX
 OS Homo sapiens.
 XX
 PN W09915553-A2.
 XX
 PD 01-APR-1999.
 XX
 PF 23-SEP-1998; 98MO-DE02896.
 XX
 PR 11-MAY-1998; 98DE-1021060.
 PR 23-SEP-1997; 97DE-1041929.
 XX
 PA (DEKO-) DEUT KOCH INST ROBERT:

PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRlich-INST.
 XX
 PI Kroczeck R;
 XX
 DR WPI: 1999-276975/23.
 DR N-PSDB: X37661.
 XX
 PT Polypeptide 8F4 co-stimulates T cells and is present only on
 PT activated cells
 XX
 PS Claim 2: Page 24; 47pp; German.
 CC
 CC This invention describes a novel human protein, 8F4, and its encoding
 CC nucleic acid which co-stimulates T cells and is present on activated CD4+
 CC and CD8+ T cells but not on resting or activated B cells, granulocytes,
 CC monocytes, natural killer or dendritic cells. 8F4 has anticancer,
 CC antiviral, anti-asthma and immunomodulatory activity. 8F4 provides a
 CC strong co-stimulatory signal for T cell activation, i.e. it amplifies
 CC proliferation of T cells, synthesis of certain cytokines and other
 CC regulatory agents, and improves T cell-dependent antibody production
 CC by B cells. Agents that inhibit 8F4 are used to treat or prevent
 CC autoimmune diseases, to prevent transplant rejection and to treat
 CC disorders of immune system regulation. 8F4, or cells that express it,
 CC is/are used to treat or prevent cancers, acquired immune deficiency
 CC syndrome, asthma and chronic infectious diseases (e.g. hepatitis B or C).
 CC
 XX
 SQ Sequence 199 AA:
 Query Match 76.8%; Score 152; DB 20; Length 199;
 Best Local Similarity 100.0%; Pred. No. 3.5e-149;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMSGIWFPLFLRLIKVLTGEINGSANVEMFIFHNGVQIICKYPIYQOEFKMLIKGQ 60
 Db 1 mksglwyfflfcrlrlkvtlgeingsanvemifhngvqilckypdivqfkmqllksgq 60
 QY 61 IICDLTKTKGSGNTWSIKSLKFCCHSOLSNNSVSFFLYNIDSHANYFCNLSIFDPPPK 120
 Db 61 IICDLTKTKGSGNTWSIKSLKFCCHSOLSNNSVSFFLYNIDSHANYFCNLSIFDPPPK 120
 QY 121 VLTGGLHYEVSQCCOLKFWLPICGAFV 152
 Db 121 vltggylhyesqccqlkfwlpigcaafv 152
 RESULT 5
 B08731
 B08731 standard; Protein: 199 AA.
 XX
 AC B08731;
 XX
 DT 02-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of a human CRP1 polypeptide.
 KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
 KW T-lymphocyte activation; type I transmembrane protein; T cell activation;
 KW T cell proliferation; T-cell mediated disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FH Peptide
 FT 1..20 Location/Qualifiers
 FT /note="signal peptide"
 FT 21..199
 FT Protein /note="mature protein"
 FT 21..140
 FT Domain /note="extracellular domain"
 FT 141..161
 FT Domain /note="predicted transmembrane domain"
 FT 162..199
 FT /note="intracellular domain"

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XX PN WO200046240-A2.
XX 10-AUG-2000.
XX
XX PF 27-JAN-2000; 2000WO-US01871.
XX PR 03-FEB-1999; 9905-0244448.
XX PR 08-MAR-1999; 9905-0264527.
XX
XX PA (AMGE-) AMGEN INC.
XX PI Yoshinaga SK;
XX DR WPI; 2000-543476/49.
XX DR N-PSDB; A64558.
XX
XX PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
XX PT in the treatment, prevention and diagnosis of T cell mediated disorders
XX
XX PS Disclosure; Fig 13A; 174pp; English.
XX
XX CC The present sequence represents a CRP1 (CD28 related protein-1)
XX CC polypeptide. The specification also describes a B7RP1 (B7 related
XX CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
XX CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
XX CC predicted to be a type I transmembrane protein. The nucleic acids are
XX CC useful for regulating T cell activation or proliferation in an animal.
XX CC The polypeptides are useful for treating, preventing ameliorating or
XX CC diagnosing a T-cell mediated disorder in an animal. They can also be
XX CC used to identify test molecules that bind to the polypeptides.
XX
XX SQ Sequence 199 AA;

```

Query Match 76.8%; Score 152; DB 21; Length 199;
 Best Local Similarity 100.0%; Pred. No. 3.5e-149;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MKSGLMWFFLECLRIKYLGTGEINSGANYEMFIFHNGGVQILCKRPDIYQOFKMLKGGQ 60
Db 1 mksglwyfflfcrltkylgtelngsanyemfifhngvqilckypdiyqgfkmlk99q 60
QY 61 ILCDLTKTKSGNTVSIKSLKFSCHSLSNNSVSFFLYNLDSHANYEFCNLSTFDPPEFK 120
Db 61 lldltktksgntvsiikslkfchsqslsnnsvsfflynlshanyefcnlstfdppfk 120
QY 121 VTLTGGYLIHTYESQLCCQLKFWMLPFGCAAFV 152
Db 121 vtltygylihtyesqlccqlkfwlpgcaafv 152

```

RESULT 6
 W71874
 ID W71874 standard; Protein; 200 AA.
 AC W71874;
 XX
 XX DT 11-DEC-1998 (first entry)
 XX
 DE Rat cell surface protein #1.
 XX
 XX Rat; cell surface protein; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 OS Rattus sp.
 XX
 XX PN WO9838216-A1.
 XX PD 03-SEP-1998.

```

PF 27-FEB-1998; 98WO-JP00837.
XX
XX PR 26-FEB-1998; 98JP-0062217.
XX PR 27-FEB-1997; 97JP-0062290.
XX
XX PA (NISR ) JAPAN TOBACCO INC.
XX PI Tamatani T, Tezuka K;
XX DR WPI; 1998-481144/41.
XX DR N-PSDB; V61357.
XX
XX PT Cell surface molecule expressed in thymocytes and lymphocytes and -
XX PT mediating signal transmission and cell adhesion, and antibodies to
XX PT it useful in treatment of auto-immune and allergic disorders.
XX
XX PS Claim 9; Page 106-109; 149pp; Japanese.
XX
XX CC The present sequence represents a rat cell surface protein which is
XX CC expressed by thymocytes and by mitogen-stimulated lymphocytes. The cell
XX CC surface protein induces adhesion of mitogen-stimulated lymphocytes to
XX CC antibodies recognising the cell surface protein. These antibodies also
XX CC produce an increase in peripheral blood lymphocytes in the presence of
XX CC an antibody recognising CD3 antigen. The cell surface protein contains
XX CC the amino acid sequence FDPPEF in its extracellular region and the
XX CC sequence YMMF in its intracellular region. The cell surface protein can
XX CC be used in the prevention and treatment of autoimmune and allergic
XX CC diseases, and in the diagnosis and investigation of such disorders.
XX
XX SQ Sequence 200 AA;

```

Query Match 8.6%; Score 17; DB 19; Length 200;
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 62 LCDLTKTKSGNTVSIK 78
Db 62 lcdltktksgntvsiik 78

```

RESULT 7
 W71875
 ID W71875 standard; Protein; 216 AA.
 AC W71875;
 XX
 XX DT 11-DEC-1998 (first entry)
 XX
 DE Rat cell surface protein #2.
 XX
 XX Rat; cell surface protein; lymphocyte; cell adhesion;
 KW signal transmission; autoimmune disorder; allergy; diagnosis;
 KW mitogen-stimulated.
 XX
 OS Rattus sp.
 XX
 XX PN WO9838216-A1.
 XX PD 03-SEP-1998.
 XX
 XX PF 27-FEB-1998; 98WO-JP00837.
 XX PR 26-FEB-1998; 98JP-0062217.
 XX PR 27-FEB-1997; 97JP-0062290.
 XX
 XX PA (NISR) JAPAN TOBACCO INC.
 XX PI Tamatani T, Tezuka K;
 XX DR WPI; 1998-481144/41.
 XX DR N-PSDB; V61358.

CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX

SO Sequence 200 AA;

Query Match 8.1%; Score 16; DB 21; Length 200;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 GGYLHIYESQLCCQLK 140
 |||||
 DB 126 ggylhysesqlccqjk 141

RESULT 10
 Y92212
 ID Y92212 standard; Protein; 200 AA.
 XX
 AC Y92212;
 XX

10-AUG-2000 (first entry)

DE Murine Th2-specific polypeptide, m1228.

XX m1288; Th2-specific; T helper cell; anti-inflammatory; antiarthritic;
 KM CD28; antidiabetic; immunosuppressive; neuroprotective; dermatological;
 KM antipsoriatic; antiallergic; antiallergic; anti-viral; ophthalmological;
 KM CTLA-4; nephrotoxic; anti-HIV; antibacterial.
 XX
 OS Mus musculus.

XX Key Location/Qualifiers

EH Peptide 114..119

FT /label="conserved_PPP_motif

FT /note="common in CD28 and CTLA-4"

FT Peptide 181..184

FT /label="YXXM_motif

FT /note="common in CD28 and CTLA-4; necessary for
 CD28-mediated phosphatidylinositol 3-kinase
 activity"

FT WO200019988-A1.

XX 13-APR-2000.

PF 06-OCT-1999; 99WO-US23156.

XX 07-OCT-1998; 98US-0168229.

PR 26-FEB-1999; 99US-0258670.

XX 06-OCT-1999; 99US-0413136.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lehar S, Manning S, Coyle AJ, Gutierrez-ramos J;

XX WPI: 2000-303619/26.

XX N-PSDB; A09054.

XX T helper (Th) 2 nucleic acids and encoded proteins, useful for the

XX diagnosis and treatment of immune and respiratory disorders such as

XX Crohn's diseases, arthritis, insulin dependent diabetes and

XX autoimmunity

XX Claim 16; Page 130-131; 159pp; English.

XX This Th2-specific polypeptide is encoded by a murine orthologue m1288.

XX The protein shares homology with both human and murine CD28 and CTLA-4.

XX A novel method for modulating a Th2 response, an immune response, or

XX suppressing airway inflammation or hyperresponsiveness in a mammal

XX comprises administering a Th2-specific polypeptide of the invention, an

XX antibody to such a polypeptide or allelic variants of the genes. The

CC novel DNA and polypeptide sequences are useful for treatment and
 CC diagnosis of Th cell and Th cell-like disorders such as Crohn's diseases,
 CC arthritis, insulin dependent diabetes, autoimmunity, multiple sclerosis,
 CC dermatitis, psoriasis, graft rejection, graft versus host diseases,
 CC sarcoidosis, asthma, allergies, conjunctivitis, glomerular nephritis,
 CC viral infections (including human immunodeficiency virus (HIV)),
 CC bacterial infections, bronchitis, cystic fibrosis, diptheria,
 CC emphysema, pneumonia, and Legionnaires disease.
 XX

SO Sequence 200 AA;

Query Match 8.1%; Score 16; DB 21; Length 200;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 GGYLHIYESQLCCQLK 140
 |||||
 DB 126 ggylhysesqlccqjk 141

RESULT 11
 R54669
 ID R54669 standard; Protein; 120 AA.
 XX
 AC R54669;
 XX

DT 12-JAN-1995 (first entry)

XX Mouse brain natriuretic peptide.

XX Brain natriuretic peptide; BNP; detection.

XX Mus musculus.

XX Key Location/Qualifiers

EH Peptide 1..75

FT /label="sig_peptide

FT Protein 76..120

FT /label="mat_protein

FT Region 1..120

FT /note="Met(-75)-Leu(45); claim 5"

FT Region 26..120

FT /note="Ser(-50)-Leu(45); claim 4"

XX JP06107688-A.

XX 19-APR-1994.

PF 29-SEP-1992; 92JP-0259488.

XX 29-SEP-1992; 92JP-0259488.

XX (SHIO) SHIONOGI & CO LTD.

XX WPI: 1994-163940/20.

XX N-PSDB; Q65357.

XX Mouse brain natriuretic peptide - useful for the detection and

XX determination of BNP

XX Disclosure; Page 7-8; 9pp; Japanese.

XX Mouse BNP can be used for the detection and the determination

XX of BNP in a sample and for the prepn. of various reagents contg.

XX BNP.

XX Query Match 3.5%; Score 7; DB 15; Length 120;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 QFKMQLL 56
 |||||
 DB 38 qfkmql 44

RESULT 12

RS4670
 ID RS4670 standard; Protein; 120 AA.

XX
 AC RS4670;

DT 12-JAN-1995 (first entry)

DE Mouse brain natriuretic peptide.

XX Brain natriuretic peptide; BNP; detection.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..75

FT /label= sig_peptide

FT Protein 76..120

FT /label= mat_protein

PN JP06107688-A.

PD 19-APR-1994.

PE 29-SEP-1992; 92JP-0259488.

PR 29-SEP-1992; 92JP-0259488.

PA (SHIO) SHIONOGI & CO LTD.

XX MPI: 1994-163940/20.

DR N-PSDB; Q65358.

XX Mouse brain natriuretic peptide - useful for the detection and

PT determination of BNP

XX Disclosure; Page 8-9; 9pp; Japanese.

PS Mouse BNP can be used for the detection and the determination

CC of BNP in a sample and for the prepn. of various reagents contg.

XX BNP.

XX Sequence 120 AA;

OY 50 QFKMQLL 56

|||||

DB 38 qfkmql 44

RESULT 13

RS4670
 ID P20107 standard; Protein; 170 AA.

XX P20107;

DT 10-AUG-1992 (first entry)

DE Sequence encoded by leukocyte interferon leif E cDNA.

XX Viral infection; therapy; malignancy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..4
 FT /label= signal

GB2079291-A.

XX 20-JAN-1992.

XX 01-JUL-1981; 81GB-0120279.

XX 21-APR-1981; 81US-0256204.

XX 01-JUL-1980; 80US-0164986.

XX 08-SEP-1980; 80US-0184909.

XX 10-NOV-1980; 80US-0205578.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX (GENE-) GENENTECH INC.

XX Goeddel DYN, Pestka S;

XX MPI: 1982-04460E/03.

XX N-PSDB; N20094.

XX Mature human leukocyte interferon polypeptide(s) - prepd. from

XX microdes transformed with appropriate DNA sequences

XX Example; Fig 4; 20pp; English.

XX The inventors claim a polypeptide comprising the AA sequence of a

XX mature human leif and a DNA sequence encoding it. Leif A-D, F, H-J

XX and encoding DNA are specifically claimed. They are natural allelic

XX variations. Leif is isolated from the leukocytes of humans with

XX chronic myelogenous leukemia, induced to produce interferon with

XX Sendai or Newcastle disease virus; esp. the cell line KG-1.

XX Sequence 170 AA;

OY 163 LTKKKYS 169

|||||

DB 135 ltkkys 141

RESULT 14

G14014

ID G14014 standard; Protein; 209 AA.

XX G14014;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 13719.

XX Protein identification; signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130049.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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Query Match 3.5%; Score 7; DB 21; Length 209;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 67 yfflcl 73

RESULT 15
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ID G59943 standard; Protein; 209 AA.
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XX G59943;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 77591.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hydrolisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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PR 05-MAR-1999; 99US-0123180.
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Query Match 3.5%; Score 7; DB 21; Length 209;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 YFFPFL 13
Db 67 yfflcl 73

Search completed: May 30, 2001, 16:52:29
Job time: 25 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:04 ; Search time 14.15 Seconds

(without alignments)
961.635 Million cell updates/sec

Title: us-09-509-283-2

Perfect score: 198
Sequence: 1 MKSGLMYFFFLCRLKRVKVG.....YMPRAVNVAKKSRIDVTL 198

Scoring table:

Gapop: 60.0 , Gapext: 60.0

Searched: 198801 seqs, 68722935 residues

Word size : 0

Total number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 152 | 76.8 | 199 | 2 | inducible T-cell c |
| 2 | 17 | 8.6 | 200 | 2 | activation-Inducib |
| 3 | 17 | 8.6 | 216 | 2 | antibiotic resist |
| 4 | 8 | 4.0 | 147 | 1 | ribosomal protei |
| 5 | 7 | 3.5 | 209 | 2 | hypothetical prote |
| 6 | 7 | 3.5 | 221 | 2 | phosphoglycolate p |
| 7 | 7 | 3.5 | 276 | 2 | probable n-acetyl |
| 8 | 7 | 3.5 | 385 | 2 | proline-rich prote |
| 9 | 10 | 3.5 | 513 | 2 | translation elonga |
| 10 | 17 | 3.5 | 558 | 2 | conserved hypothet |
| 11 | 12 | 3.5 | 605 | 2 | hypothetical prote |
| 12 | 13 | 3.5 | 907 | 2 | inter-alpha-trypsi |
| 13 | 14 | 3.5 | 1047 | 2 | probable translati |
| 14 | 15 | 3.5 | 1291 | 2 | hypothetical prote |
| 15 | 16 | 3.5 | 1361 | 2 | S-layer protein - |
| 16 | 17 | 3.5 | 1466 | 2 | ATP-binding cass |
| 17 | 18 | 3.5 | 1766 | 2 | 14k protein - pea |
| 18 | 19 | 3.5 | 4151 | 2 | groovin gene prote |
| 19 | 20 | 3.0 | 32 | 2 | hypothetical prote |
| 20 | 21 | 3.0 | 72 | 2 | ribosomal protein |
| 21 | 22 | 3.0 | 82 | 2 | M-like protein em |
| 22 | 23 | 3.0 | 85 | 2 | hypothetical prote |
| 23 | 24 | 3.0 | 98 | 2 | single strand DNA- |
| 24 | 25 | 3.0 | 99 | 2 | probable transpos |
| 25 | 26 | 3.0 | 99 | 2 | Ig epsilon chain C |
| 26 | 27 | 3.0 | 100 | 2 | hypothetical CRF-1 |
| 27 | 28 | 3.0 | 102 | 2 | serotonin receptor |
| 28 | 29 | 3.0 | 110 | 2 | T-cell receptor al |

| | | | | | | |
|----|---|-----|-----|---|--------|--------------------|
| 30 | 6 | 3.0 | 113 | 2 | 549881 | Tcell receptor alp |
| 31 | 6 | 3.0 | 113 | 2 | 725658 | hypothetical prote |
| 32 | 6 | 3.0 | 115 | 2 | E53116 | Ig epsilon chain C |
| 33 | 6 | 3.0 | 121 | 2 | T24096 | hypothetical prote |
| 34 | 6 | 3.0 | 126 | 2 | C53116 | Ig epsilon chain C |
| 35 | 6 | 3.0 | 129 | 2 | T50446 | conserved hypothet |
| 36 | 6 | 3.0 | 130 | 2 | S67024 | probable membrane |
| 37 | 6 | 3.0 | 135 | 2 | E71413 | ribosomal protein |
| 38 | 6 | 3.0 | 135 | 2 | T06426 | ribosomal protein |
| 39 | 6 | 3.0 | 135 | 2 | T06430 | ribosomal protein |
| 40 | 6 | 3.0 | 135 | 2 | T06431 | ribosomal protein |
| 41 | 6 | 3.0 | 135 | 2 | T06451 | ribosomal protein |
| 42 | 6 | 3.0 | 135 | 2 | B70456 | thioredoxin - Aqu |
| 43 | 6 | 3.0 | 138 | 2 | E81045 | hypothetical prote |
| 44 | 6 | 3.0 | 150 | 2 | D46036 | galactosyltransfer |
| 45 | 6 | 3.0 | 153 | 2 | B69033 | conserved hypothet |

ALIGNMENTS

| RESULT | 1 | Score | Match | Length | DB ID | Description |
|---|---|---------------------|------------|-------------|--------|--------------------|
| 78540 | inducible T-cell co-stimulator ICOS precursor - human | 76.8% | 152 | 199 | 2 | inducible T-cell c |
| C:Species: Homo sapiens (man) | | | | | | |
| C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 07-May-1999 | | | | | | |
| C:Accession: S78540; S78748; S78749 | | | | | | |
| R:Krocsek, R. | | | | | | |
| submitted to the Protein Sequence Database, June 1998 | | | | | | |
| A:Reference number: S78540 | | | | | | |
| A:Accession: S78540 | | | | | | |
| A:Molecule type: mRNA | | | | | | |
| A:Residues: 1-199 <KRO> | | | | | | |
| A:Experimental source: cell line MOLT-4V | | | | | | |
| R:Hutloff, A.; Dittlich, A.M.; Beler, K.C.; Eljaschewitsch, B.; Kraft, R.; Anagnostop | | | | | | |
| Nature 397, 263-266, 1999 | | | | | | |
| A:title: ICOS is an inducible T-cell co-stimulator structurally and functionally rela | | | | | | |
| A:Reference number: S78748; MUID:99127892 | | | | | | |
| A:Accession: S78748 | | | | | | |
| A:Molecule type: mRNA | | | | | | |
| A:Residues: 1-199 <HUT1> | | | | | | |
| A:Experimental source: cell line MOLT-4V | | | | | | |
| A:Accession: S78749 | | | | | | |
| A:Molecule type: protein | | | | | | |
| A:Residues: 'X', 193-198 <HUT2> | | | | | | |
| A:Experimental source: cell line MOLT-4V | | | | | | |
| C:Complex: homodimer | | | | | | |
| C:Superfamily: immunoglobulin homology | | | | | | |
| C:Keywords: dimer; glycoprotein; T-cell; transmembrane protein | | | | | | |
| F:1-19/Domains: (or 1-20) signal sequence #status predicted <SIG> | | | | | | |
| F:20-199/Product: (or 21-199) inducible costimulator ICOS #status predicted <MAT> | | | | | | |
| F:21-138/Domains: extracellular #status predicted <EXT> | | | | | | |
| F:26-132/Domains: immunoglobulin homology <IMM> | | | | | | |
| F:139-164/Domains: transmembrane #status predicted <TM> | | | | | | |
| F:165-199/Domains: intracellular #status predicted <INT> | | | | | | |
| F:23,89,110/Binding site: carbohydrate (asn) (covalent) #status predicted | | | | | | |
| Query Match | 76.8% | Score 152; | DB 2; | Length 199; | | |
| Best local similarity | 100.0% | Pred. No. 2,1e-155; | | | | |
| Matches 152; | Conservative | 0; | Mismatches | 0; | Indels | 0; |
| DB | 1 | 1 | 1 | 1 | 1 | 1 |
| QY | 1 | 1 | 1 | 1 | 1 | 1 |
| DB | 1 | 1 | 1 | 1 | 1 | 1 |
| QY | 61 | 11 | 11 | 11 | 11 | 11 |
| DB | 61 | 11 | 11 | 11 | 11 | 11 |
| QY | 121 | 11 | 11 | 11 | 11 | 11 |
| DB | 121 | 11 | 11 | 11 | 11 | 11 |

RESULT 2
JC7397
activation-inducible lymphocyte immuno-mediatory molecule-2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000
C:Accession: JC7397; PC7100
R:Rezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, B.
Biochem. Biophys. Res. Commun. 276, 335-345, 2000
A:Title: Identification and characterization of rat AILM/ICOS, a novel T-cell costimulatory molecule
A:Reference number: JC7396
A:Contents: Spleen
A:Accession: JC7397
A:Molecule type: mRNA
A:Residues: 1-200 <TE2>
A:Cross-references: DDBJ:AB023134
A:Accession: PC7100
A:Molecule type: protein
A:Residues: 21-40 <TE2>
C:Comment: This protein is an inducible cell surface glycoprotein, and a type I transmembrane protein, and plays an important role for the maturation or selection of T cells in thymus.
C:Genetics:
C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 8.6%; Score 17; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LCDLTKTKSGNTVSIK 78
|||||
Db 62 LCDLTKTKSGNTVSIK 78

RESULT 3
JC7396
activation-inducible lymphocyte immuno-mediatory molecule-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 17-Nov-2000
C:Accession: JC7396; PC7099
R:Rezuka, K.; Tsuji, T.; Hirano, D.; Tamatani, T.; Sakamaki, K.; Kobayashi, Y.; Kamada, B.
Biochem. Biophys. Res. Commun. 276, 335-345, 2000
A:Title: Identification and characterization of rat AILM/ICOS, a novel T-cell costimulatory molecule
A:Reference number: JC7396
A:Contents: Spleen
A:Accession: JC7396
A:Molecule type: mRNA
A:Residues: 1-216 <TE2>
A:Cross-references: DDBJ:AB023133
A:Accession: PC7099
A:Molecule type: protein
A:Residues: 21-40 <TE2>
C:Comment: This protein is an inducible cell surface glycoprotein, and a type I transmembrane protein, and plays an important role for the maturation or selection of T cells in thymus.
C:Genetics:
A:Gene: ailm-1
C:Keywords: glycoprotein; T-cell; transmembrane protein

Query Match 8.6%; Score 17; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 LCDLTKTKSGNTVSIK 78
|||||
Db 62 LCDLTKTKSGNTVSIK 78

RESULT 4
H69779
antibiotic resistance protein homolog ydfB - Bacillus subtilis

C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: H69779
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: H69779
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Ber A.; Ehlich, S.D.; Emmerson, P.T.; Entian, K.D.; Erlington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallazzi, A.; Gal lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huillo, M Koeter, P.; Konigsdorf, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Pario, V.; Pohl, T.M.; Portele Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl A:Authors: Schleich, S.; Schreier, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akewich, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; M0ID:98044033
A:Accession: H69779
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <KUN>
A:Cross-references: GB:299106; GB:AL009126; NID:g2632653; PIDN:CAB12342.1; PID:g26328 A:Experimental source: strain 168
C:Genetics:
C:Gene: ydfB
C:Superfamily: probable antibiotic resistance protein ydfB

Query Match 4.0%; Score 8; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 LTKKKYSS 170
|||||
Db 7 LTKKKYSS 14

RESULT 5
R3HS12
ribosomal protein S19.er [validated] - Halocaula marismortui
N:Alternate names: ribosomal protein E1.3; ribosomal protein HS12
C:Species: Halocaula marismortui
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 04-Feb-2000
C:Accession: S00183; C24304
R:Kimura, J.; Arndt, E.; Kimura, M.
FEBS Lett. 224, 65-70, 1987
A:Title: Primary structures of three highly acidic ribosomal proteins S6, S12 and S15
A:Reference number: S00182; M0ID:88055606
A:Accession: S00183
A:Molecule type: protein
A:Residues: 1-147 <KIM>
A:Note: the source is designated as Halobacterium marismortui
R:Shoham, M.; Dijk, J.; Reinhardt, R.; Wiltmann-Liebold, B.
FEBS Lett. 204, 323-330, 1986
A:Title: Purification and characterization of ribosomal proteins from the 30 S subunit
A:Reference number: A24304
A:Accession: C24304
A:Molecule type: protein
A:Residues: 1-11, 'E', '13-14', '1', '16-18', '1', '20-21' <SHO>
A:Note: the source is designated as Halobacterium marismortui
C:Superfamily: rat ribosomal protein S19
C:Keywords: protein biosynthesis; ribosome

Query Match 3.5%; Score 7; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 KTKGSGN 73
|||||

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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:49 ; Search time 9.63 Seconds
(without alignments) 704.318 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 198

Sequence: 1 MNSGLMYFFLFCLIRKVLTVG.....YMFRAVNTAKSRSLTDVTL 198

Scoring table: OLIGO

Seatched: 93435 seqs, 34255486 residues

Word size: 0

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 7 | 3.5 | 147 | 1 | R19E_HALMA |
| 2 | 7 | 3.5 | 907 | 1 | I19E_MOUSE |
| 3 | 6 | 3.0 | 72 | 1 | RL28_THEMA |
| 4 | 6 | 3.0 | 100 | 1 | NU1M_PHYIN |
| 5 | 6 | 3.0 | 121 | 1 | TH1L_GAEEL |
| 6 | 6 | 3.0 | 135 | 1 | RL27_ARATH |
| 7 | 6 | 3.0 | 135 | 1 | RL27_PEA |
| 8 | 6 | 3.0 | 139 | 1 | RPB6_ASFEM2 |
| 9 | 6 | 3.0 | 147 | 1 | RPB6_ASFEM2 |
| 10 | 6 | 3.0 | 160 | 1 | FMA3_ECOLI |
| 11 | 6 | 3.0 | 160 | 1 | FMDR_ECOLI |
| 12 | 6 | 3.0 | 179 | 1 | YAIL_ECOLI |
| 13 | 6 | 3.0 | 179 | 1 | YFCP_ECOLI |
| 14 | 6 | 3.0 | 186 | 1 | YCEB_ECOLI |
| 15 | 6 | 3.0 | 189 | 1 | BBP_PIEBR |
| 16 | 6 | 3.0 | 189 | 1 | RPOE_HAETIN |
| 17 | 6 | 3.0 | 191 | 1 | RL9A_YEAST |
| 18 | 6 | 3.0 | 191 | 1 | RL9B_YEAST |
| 19 | 6 | 3.0 | 191 | 1 | RPOE_ECOLI |
| 20 | 6 | 3.0 | 191 | 1 | RPOE_ECOLI |
| 21 | 6 | 3.0 | 214 | 1 | RMS2_NICAL |
| 22 | 6 | 3.0 | 237 | 1 | Y450_MYCPN |
| 23 | 6 | 3.0 | 240 | 1 | NESA_ECOLI |
| 24 | 6 | 3.0 | 241 | 1 | YMO8_PARTE |
| 25 | 6 | 3.0 | 247 | 1 | TRY4_RAT |
| 26 | 6 | 3.0 | 248 | 1 | YMT1_INBAC |
| 27 | 6 | 3.0 | 262 | 1 | FHUF_ECOLI |
| 28 | 6 | 3.0 | 274 | 1 | YBLG_SCHPO |
| 29 | 6 | 3.0 | 286 | 1 | ISPE_BUCAI |
| 30 | 6 | 3.0 | 287 | 1 | RN07_SCHPO |
| 31 | 6 | 3.0 | 291 | 1 | SFAH_ECOLI |
| 32 | 6 | 3.0 | 304 | 1 | CAHH_VACCC |
| 33 | 6 | 3.0 | 304 | 1 | CAHH_VACCV |

| | | | | | |
|----|---|-----|-----|---|-------------|
| 34 | 6 | 3.0 | 304 | 1 | CAHH_VARY |
| 35 | 6 | 3.0 | 306 | 1 | RCHEM_RHOCA |
| 36 | 6 | 3.0 | 307 | 1 | RCHEM_RHOSH |
| 37 | 6 | 3.0 | 313 | 1 | NU2M_RHISA |
| 38 | 6 | 3.0 | 320 | 1 | YB9K_YEAST |
| 39 | 6 | 3.0 | 324 | 1 | MAS_MOUSE |
| 40 | 6 | 3.0 | 324 | 1 | MAS_RAT |
| 41 | 6 | 3.0 | 343 | 1 | FPPS_ARTAN |
| 42 | 6 | 3.0 | 346 | 1 | YC54_SYNY3 |
| 43 | 6 | 3.0 | 356 | 1 | KARG_SCHAM |
| 44 | 6 | 3.0 | 358 | 1 | GLPO_ECOLI |
| 45 | 6 | 3.0 | 359 | 1 | ODPB_PEA |

ALIGNMENTS

| | |
|--|----------------------------------|
| RESULT 1 | |
| ID R19E_HALMA | STANDARD: PRT: 147 AA. |
| AC P19952: | |
| DT 01-FEB-1991 (Rel. 17, Created) | |
| DT 01-FEB-1991 (Rel. 17, Last sequence update) | |
| DT 30-MAY-2000 (Rel. 39, Last annotation update) | |
| DE 30S RIBOSOMAL PROTEIN S19E (HS12) (EL.3). | |
| GN RPS19E. | |
| OS Halobacterium marismortui (Halobacterium marismortui). | |
| OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Halobacterium. | |
| OX NCBI_TaxID=2238; | |
| RN [1] | |
| RP SEQUENCE. | |
| RX MEDLINE=86055606; PubMed=3315748; | |
| RA Kimura J., Arndt E., Kimura M.; | |
| RT "Primary structures of three highly acidic ribosomal proteins S6, S12 and S15 from the archaebacterium Halobacterium marismortui."; | |
| RL FEBS Lett. 224:65-70(1987). | |
| RN [2] | |
| RP SEQUENCE OF 1-21. | |
| RA Shoham M., Dijk J., Reinhardt R., Wiltmann-Liebold B.; | |
| RT "Purification and characterization of ribosomal proteins from the 30S subunit of the extreme halophile Halobacterium marismortui."; | |
| RL FEBS Lett. 204:323-330(1986). | |
| CC -1- SIMILARITY: BELONGS TO THE S19E FAMILY OF RIBOSOMAL PROTEINS. | |
| DR PIR: S00183; R3HS12. | |
| DR InterPro: IPR001266; .. | |
| DR Pfam: PF01090; Ribosomal_S19e; 1. | |
| DR PROSITE: PS00628; RIBOSOMAL_S19E; 1. | |
| KW Ribosomal protein. | |
| FT CONFLICT 12 I -> E (IN REF. 2). | |
| FT CONFLICT 15 L -> I (IN REF. 2). | |
| FT CONFLICT 19 L -> I (IN REF. 2). | |
| SO SEQUENCE 147 AA; 16438 MW; 8F66327D14530FE CRC64; | |
| Query Match | 3.5%; Score 7; DB 1; Length 147; |
| Best Local Similarity | 100.0%; Pred. No. 4; |
| Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY 67 KTKGSGN 73 | |
| DB 87 KTKGSGN 93 | |
| RESULT 2 | |
| ID ITH1_MOUSE | STANDARD: PRT: 907 AA. |
| AC O61702: | |
| DT 15-JUL-1998 (Rel. 36, Created) | |
| DT 15-JUL-1998 (Rel. 36, Last sequence update) | |
| DT 01-OCT-2000 (Rel. 40, Last annotation update) | |
| DE INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H1 PRECURSOR (ITI HEAVY CHAIN H1). | |
| GN ITH1. | |

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6N; TISSUE=Liver;
 RX MEDLINE=95194326; PubMed=7534067;
 RA Chan P., Risler J.-L., Raguenez G., Sallier J.-P.;
 RT "The three heavy-chain precursors for the inter-alpha-inhibitor family
 in mouse: new members of the multicopper oxidase protein group with
 differential transcription in liver and brain";
 RL Biochem. J. 306:505-512(1995).
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURON WHICH ARE
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
 CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
 CC -1- TISSUE SPECIFICITY: LIVER-SPECIFIC.
 CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WFMA DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X70391; CAA49841.1; -
 CC DR MDG; MG1:96618; Itih1.
 CC DR InterPro: IPR002035; -
 CC DR Pfam: PF000692; wfa_1.
 CC DR PROSITE: PS50234; WFMA_DOMAIN: 1.
 CC KW Serine protease inhibitor; Repeat; Signal; Multigene family;
 CC Glycoprotein.
 CC FT SIGNAL 1 26
 CC FT CHAIN 27 668
 CC FT POTENTIAL.
 CC FT INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
 CC FT H1
 CC FT POTENTIAL.
 CC FT PROPER 669 907
 CC FT DOMAIN 287 447
 CC FT CARBOHYD 282 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 585 585 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT BINDING 668 668 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
 CC FT (BY SIMILARITY).
 CC SQ SEQUENCE 907 AA; 101082 MW; FE7FD/6500CAF3BC CRC64;
 CC -----
 CC Query Match 3.5%; Score 7; DB 1; Length 907;
 CC Best Local Similarity 100.0%; Pred. No. 20;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S RIBOSOMAL PROTEIN L28.
 OS GN
 RN RPMB OR TM0255.
 OC Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwynn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima";
 RL Nature 399:323-329(1999).
 CC -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AE001708; AAD35344.1; -
 CC DR TIGR: TM0255; -
 CC DR InterPro: IPR001383; -
 CC DR Pfam: PF008830; Ribosomal_L28; 1.
 CC KW Ribosomal protein.
 CC SQ SEQUENCE 72 AA; 8052 MW; A18B09B0F9F76B49 CRC64;
 CC -----
 CC Query Match 3.0%; Score 6; DB 1; Length 72;
 CC Best Local Similarity 100.0%; Pred. No. 26;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71 SGNVTS 76
 DB 16 SGNVTS 21

RESULT 4
 ID NULM_PHYIN STANDARD; PRT; 100 AA.
 AC 037598;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).
 GN ND4L OR NAD4L.
 OS Phytochthora infestans (Potato late blight fungus).
 OS Mitochondrion.
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 OC Phytochthora.
 OX NCBI_TaxID=4787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 16981;
 RA Chesnick J.M., Tuxbury K., Coleman A., Burger G., Lang B.F.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE + NAD(+) + UBIQUINOL.
 CC -----
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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:34 ; Search time 22.71 Seconds

(without alignments)
1021.892 Million cell updates/sec

Title: US-09-509-283-2

Sequence: 1 MMSGLMYFFFLCRLKRVLTG.....YMFRAVNTAKKSRLTDTVL 198

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 374700 seqs, 117207915 residues

Word size : 0

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL.15:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.unclassified:*
13: sp.vertebrate:*
14: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 152 | 76.8 | 199 | 4 | O9Y6W8 homo sapien |
| 2 | 152 | 8.6 | 200 | 4 | O9R1T7 |
| 3 | 17 | 8.6 | 216 | 11 | O9WVR9 |
| 4 | 16 | 8.1 | 200 | 11 | O9WVS0 |
| 5 | 16 | 8.1 | 200 | 11 | O9JL17 |
| 6 | 8 | 4.0 | 261 | 2 | P96679 |
| 7 | 8 | 4.0 | 1243 | 2 | O9RDG5 |
| 8 | 8 | 3.5 | 108 | 5 | O9V7Z6 |
| 9 | 7 | 3.5 | 173 | 9 | O38610 |
| 10 | 7 | 3.5 | 209 | 10 | O9SWC9 |
| 11 | 7 | 3.5 | 221 | 2 | P73525 |
| 12 | 7 | 3.5 | 309 | 14 | O72512 |
| 13 | 7 | 3.5 | 309 | 14 | O71309 |
| 14 | 7 | 3.5 | 359 | 13 | O9IBP8 |
| 15 | 7 | 3.5 | 385 | 14 | O41160 |
| 16 | 7 | 3.5 | 387 | 13 | O9IBG0 |
| 17 | 7 | 3.5 | 471 | 14 | O84697 |
| 18 | 7 | 3.5 | 513 | 3 | O9UUL5 |
| 19 | 7 | 3.5 | 549 | 5 | O24204 |

| | | | | | | |
|----|---|-----|------|----|--------|---------------------|
| 20 | 7 | 3.5 | 558 | 2 | O9PKV6 | O9PKV6 chlamydia m |
| 21 | 7 | 3.5 | 605 | 2 | O83607 | O83607 treponema p |
| 22 | 7 | 3.5 | 817 | 5 | O9VZJ5 | O9VZJ5 drosophila |
| 23 | 7 | 3.5 | 962 | 3 | O14437 | O14437 uromyces fa |
| 24 | 7 | 3.5 | 997 | 3 | O74242 | O74242 cryptococcu |
| 25 | 7 | 3.5 | 998 | 3 | O9UR20 | O9UR20 cryptococcu |
| 26 | 7 | 3.5 | 1047 | 3 | O94489 | O94489 schizosacch |
| 27 | 7 | 3.5 | 1152 | 4 | O9NUR2 | O9NUR2 homo sapien |
| 28 | 7 | 3.5 | 1291 | 10 | O9S054 | O9S054 arabidopsis |
| 29 | 7 | 3.5 | 1319 | 4 | O94885 | O94885 homo sapien |
| 30 | 7 | 3.5 | 1361 | 2 | O30524 | O30524 wolfinella r |
| 31 | 7 | 3.5 | 1361 | 2 | O87083 | O87083 wolfinella r |
| 32 | 7 | 3.5 | 1466 | 3 | P78576 | P78576 emericella |
| 33 | 7 | 3.5 | 1766 | 14 | O9WJD8 | O9WJD8 pea early b |
| 34 | 7 | 3.5 | 4151 | 5 | O96936 | O96936 drosophila |
| 35 | 7 | 3.5 | 4625 | 10 | O9SMH3 | O9SMH3 chlamydomon |
| 36 | 7 | 3.5 | 5201 | 5 | O9U479 | O9U479 drosophila |
| 37 | 7 | 3.5 | 5293 | 5 | O9V6V2 | O9V6V2 drosophila |
| 38 | 7 | 3.5 | 5385 | 5 | O9V6V3 | O9V6V3 drosophila |
| 39 | 6 | 3.0 | 32 | 2 | O50861 | O50861 borrelia bu |
| 40 | 6 | 3.0 | 79 | 2 | O9X9G0 | O9X9G0 yersinia bu |
| 41 | 6 | 3.0 | 79 | 14 | O04252 | O04252 human papil |
| 42 | 6 | 3.0 | 82 | 2 | O54656 | O54656 streptococc |
| 43 | 6 | 3.0 | 87 | 2 | O55319 | O55319 streptococc |
| 44 | 6 | 3.0 | 92 | 14 | O9JEN0 | O9JEN0 human immun |
| 45 | 6 | 3.0 | 93 | 10 | O9SQW7 | O9SQW7 arabidopsis |

ALIGNMENTS

| RESULT | 1 | PRELIMINARY: | PRT: | 199 AA. |
|--------|--|--------------|------|---------|
| O9Y6W8 | O9Y6W8 | | | |
| AC | O9Y6W8 | | | |
| DT | 01-NOV-1999 (TREMBLrel. 12, Created) | | | |
| DT | 01-NOV-1999 (TREMBLrel. 12, Last sequence update) | | | |
| DT | 01-NOV-1999 (TREMBLrel. 12, Last annotation update) | | | |
| DE | ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE ALLIM | | | |
| DE | PRECURSOR. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=BLOOD; | | | |
| RA | Tezuka K.; Tamatani T.; | | | |
| RT | "Cell surface molecule mediating cell adhesion and signal | | | |
| RT | transmission." | | | |
| RL | Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AB023135; BAA62129.1; - | | | |
| KW | Signal. | | | |
| FT | SIGNAL. | | | |
| SQ | SEQUENCE 199 AA; 22624 MW; 214EC741C9BDC9FC CRC64; | | | |

Query Match 76.8%; Score 152; DB 4; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.4e-156;
Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | |
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| OY | 1 | MMSGLMYFFFLCRLKRVLTGELNGSANTEMFTHNGGVQIILCKYDIYQOQFMOLLKGGQ 60 |
| DB | 1 | MMSGLMYFFFLCRLKRVLTGELNGSANTEMFTHNGGVQIILCKYDIYQOQFMOLLKGGQ 60 |
| OY | 61 | IICDLTKRGSGNTVSISLKFCHSOLSNNSVSFLYVNDHSHAVYFCNLSIFPPPPFK 120 |
| DB | 61 | IICDLTKRGSGNTVSISLKFCHSOLSNNSVSFLYVNDHSHAVYFCNLSIFPPPPFK 120 |
| OY | 121 | VLTGGLYTHYESQLCCQLKFWLPITGCAAFV 152 |
| DB | 121 | VLTGGLYTHYESQLCCQLKFWLPITGCAAFV 152 |

RESULT 2
Q9JL17 PRELIMINARY; PRT; 200 AA.
ID 09JL17
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE ALLIM
DE PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
transmission."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB023134; BAA82128.1; -
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 200 AA: 22529 MW: 0A74C3581F129D4 CRC64;

Query Match 8.6%; Score 17; DB 11; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 LCDLTKKSGGNTVSIK 78
Db 62 LCDLTKKSGGNTVSIK 78

RESULT 3
Q9WVR9 PRELIMINARY; PRT; 216 AA.
ID 09WVR9
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE ALLIM
DE PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
transmission."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB023133; BAA82127.1; -
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 216 AA: 24260 MW: 772E01320982B15A CRC64;

Query Match 8.6%; Score 17; DB 11; Length 216;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 LCDLTKKSGGNTVSIK 78
Db 62 LCDLTKKSGGNTVSIK 78

RESULT 4
Q9WVS0 PRELIMINARY; PRT; 200 AA.
ID 09WVS0

Q9WVS0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ACTIVATION-INDUCIBLE LYMPHOCYTE IMMUNOMEDIATORY MOLECULE ALLIM
DE PRECURSOR (CCLP PRECURSOR) (SURFACE PROTEIN).
GN CCPLP OR ICOS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Tezuka K., Tamatani T.;
RT "Cell surface molecule mediating cell adhesion and signal
transmission."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Wu D., Giannoni M.A., Kiesecker C.L., Faas S.J., Mickle A.P.,
RA Matis L.A., Rother R.P.;
RT "CCPLP, A novel molecule that regulates T cell activation."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RA Mages H.W., Hurlhoff A., Heuck C., Buchner K., Himmelbauer H.,
RA Oliveri F., Kroccek R.A.;
RT "Molecular cloning and characterization of murine ICOS and
RT Identification of B7h as ICOS ligand."
RL Eur. J. Immunol. 30:1040-1047(2000).
DR EMBL; AB023132; BAA82126.1; -
DR EMBL; AF257230; AAF70099.1; -
DR EMBL; AJ250559; CAB71153.1; -
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 200 AA: 22690 MW: 9B2278E4CAB1DB47 CRC64;

Query Match 8.1%; Score 16; DB 11; Length 200;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 GGYLIYESOLCCOLK 140
Db 126 GGYLIYESOLCCOLK 141

RESULT 5
Q9JL17 PRELIMINARY; PRT; 200 AA.
ID 09JL17
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE CD28-RELATED PROTEIN 1 (FRAGMENT).
DE CD28-RELATED PROTEIN 1 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINAL INTRA-EPITHELIUM;
RA Yoshinaga S.K., Whorlskey J.S., Khare S.D., Samlento U., Guo J.,
RA Horan T., Shih G., Zhang M., Cocchia M.A., Kohno T., Tafuri-Bladt A.,
RA Campbell P., Chang D., Chiu L., Dai T., Duncan G., Elliott G.S.,
RA Hui A., McCabe S.M., Scully S., Shaklee C.L., Van G., Mak T.W.,
RA Senaldi G.;
RT "T-cell co-stimulation through B7RP-1 and ICOS."
RL Nature 0:0-0(2000)
DR EMBL; AF216748; AAF45150.1; -

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 30, 2001, 16:52:04 ; Search time 12.96 Seconds
(without alignments)
293.499 Million cell updates/sec

Title: US-09-509-283-2

Perfect score: 198

Sequence: 1 MKSGLMYFFLCRLRIKVLGT.....YMFMAVNTAKKSLRDVTL 198

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 185757 seqs, 19210857 residues

Word size : 0

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|---------------------|
| 1 | 6 | 3.0 | 8 | 1 US-08-480-505-4 | Sequence 4, Appli |
| 2 | 6 | 3.0 | 9 | 1 US-08-480-505-5 | Sequence 5, Appli |
| 3 | 6 | 3.0 | 9 | 1 US-08-480-505-8 | Sequence 8, Appli |
| 4 | 6 | 3.0 | 10 | 1 US-08-480-505-6 | Sequence 6, Appli |
| 5 | 6 | 3.0 | 10 | 1 US-08-446-692-79 | Sequence 79, Appli |
| 6 | 6 | 3.0 | 10 | 1 US-08-244-496-79 | Sequence 79, Appli |
| 7 | 6 | 3.0 | 10 | 2 US-08-488-351A-79 | Sequence 79, Appli |
| 8 | 6 | 3.0 | 10 | 2 US-08-817-933A-2 | Sequence 2, Appli |
| 9 | 6 | 3.0 | 11 | 1 US-08-480-505-1 | Sequence 1, Appli |
| 10 | 6 | 3.0 | 12 | 1 US-08-480-505-7 | Sequence 7, Appli |
| 11 | 6 | 3.0 | 30 | 2 US-08-408-858A-8 | Sequence 8, Appli |
| 12 | 6 | 3.0 | 45 | 1 US-08-446-692-103 | Sequence 103, Appli |
| 13 | 6 | 3.0 | 45 | 1 US-08-446-692-104 | Sequence 104, Appli |
| 14 | 6 | 3.0 | 45 | 2 US-08-488-351A-103 | Sequence 103, Appli |
| 15 | 6 | 3.0 | 45 | 2 US-08-488-351A-104 | Sequence 104, Appli |
| 16 | 6 | 3.0 | 65 | 3 US-08-331-625A-39 | Sequence 39, Appli |
| 17 | 6 | 3.0 | 108 | 6 5284931-5 | Patent No. 5284931 |
| 18 | 6 | 3.0 | 109 | 1 US-08-037-579A-2 | Sequence 2, Appli |
| 19 | 6 | 3.0 | 109 | 3 US-08-601-184-2 | Sequence 2, Appli |
| 20 | 6 | 3.0 | 110 | 1 US-08-399-106A-6 | Sequence 6, Appli |
| 21 | 6 | 3.0 | 110 | 1 US-08-433-105A-6 | Sequence 6, Appli |
| 22 | 6 | 3.0 | 110 | 2 US-08-434-869A-6 | Sequence 6, Appli |
| 23 | 6 | 3.0 | 178 | 4 US-09-147-928-4 | Sequence 4, Appli |
| 24 | 6 | 3.0 | 194 | 2 US-08-272-255-20 | Sequence 20, Appli |
| 25 | 6 | 3.0 | 194 | 5 PCT-US95-08565-20 | Sequence 20, Appli |
| 26 | 6 | 3.0 | 203 | 3 US-08-331-625A-11 | Sequence 11, Appli |
| 27 | 6 | 3.0 | 235 | 1 US-08-015-986A-13 | Sequence 13, Appli |

28 6 3.0 235 2 US-08-446-363-13 Sequence 13, Appli
29 6 3.0 318 6 5242798-5 Patent No. 5242798
30 6 3.0 327 1 US-08-118-270-29 Sequence 29, Appli
31 6 3.0 327 5 PCT-US93-08528-29 Sequence 29, Appli
32 6 3.0 332 3 US-09-183-253-4 Sequence 4, Appli
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35 6 3.0 358 2 US-08-973-145-4 Sequence 4, Appli
36 6 3.0 358 5 PCT-US96-08081-4 Sequence 5, Appli
37 6 3.0 375 1 US-08-370-542-5 Sequence 5, Appli
38 6 3.0 375 3 US-08-542-358-5 Sequence 5, Appli
39 6 3.0 375 3 US-09-018-351-5 Sequence 5, Appli
40 6 3.0 376 1 US-07-817-920-5 Sequence 5, Appli
41 6 3.0 376 1 US-08-117-006-5 Sequence 5, Appli
42 6 3.0 376 1 US-08-216-594-5 Sequence 5, Appli
43 6 3.0 376 5 PCT-US93-00149-5 Sequence 5, Appli
44 6 3.0 377 2 US-08-461-812-2 Sequence 2, Appli
45 6 3.0 377 2 US-08-157-185-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-08-480-505-4
; Sequence 4, Application US/08480505
; Patent No. 5601821
; GENERAL INFORMATION:
; APPLICANT: STANWORTH, DENIS R
; APPLICANT: LEWIN, IAN V
; APPLICANT: NAYYAR, SARITA
; APPLICANT: JONES, VALERIE
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-3360
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,505
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,692
; FILING DATE:
; APPLICATION NUMBER: US 07/776,380
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: GB 8913737.6
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB90/00926
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 875-0400
; TELEFAX: (703) 525-3468
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-480-505-4

Query Match 3.0%; Score 6; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 KTKGSG 72
Db 1 KTKGSG 6

RESULT 2

US-08-480-505-5
; Sequence 5, Application US/08480505
; Patent No. 5601821
; GENERAL INFORMATION:
; APPLICANT: STANWORTH, DENIS R
; APPLICANT: LEWIN, IAN V
; APPLICANT: NAYYAR, SARITA
; APPLICANT: JONES, VALERIE
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-3360
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,505
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,692
; FILING DATE:
; APPLICATION NUMBER: US 07/776,380
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: GB 8913737.6
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB90/00926
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 875-0400
; TELEFAX: (703) 525-3468
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-480-505-5

Query Match 3.0%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 KTKGSG 72
Db 2 KTKGSG 7

RESULT 3

US-08-480-505-8
; Sequence 8, Application US/08480505
; Patent No. 5601821
; GENERAL INFORMATION:
; APPLICANT: STANWORTH, DENIS R
; APPLICANT: LEWIN, IAN V
; APPLICANT: NAYYAR, SARITA
; APPLICANT: JONES, VALERIE
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-3360
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,505
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,692
; FILING DATE:
; APPLICATION NUMBER: US 07/776,380
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: GB 8913737.6
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB90/00926
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 604-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 875-0400
; TELEFAX: (703) 525-3468
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-480-505-8

Query Match 3.0%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 KTKGSG 72
Db 1 KTKGSG 6

RESULT 4